

# SEQUENCE LISTING

<110> Kleanthous, Harold  
Al-Garawi, Amal  
Miller, Charles  
Tomb, Jean Francois  
Oomen, Raymond P.

<120> IDENTIFICATION OF POLYNUCLEOTIDES  
ENCODING NOVEL HELICOBACTER POLYPEPTIDES IN THE HELICOBACTER  
GENOME

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<141> 1997-06-24

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Asn Arg Val Val Ser Ser Leu Ala Ile Leu Phe Ile Ile Ile Gly Leu	
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Val Leu Met Leu Gln Ala Cys Thr Cys Pro Asn Thr Ser Gln Arg Asn		
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Tyr Ile Thr Gln Gly Val Asp Ser Ser His Ile Val Asp Gly Lys Lys		
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Thr Glu Glu Ile Glu Lys Ile Ala Thr Lys Arg Ala Thr Ile Arg Val		
70 75 80		
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Ala Gln Asn Ile Val His Lys Leu Lys Glu Ala Tyr Leu Ser Lys Thr		
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09095913 062901



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Leu	Phe	Phe	Phe 885	Phe	Phe	Ile	Phe	Phe	Lys 890	Val	Trp	Trp	Ser	Leu	Gln 895	
Glu	Glu	Leu	Glu 900	Glu	Glu	Tyr	Arg	Arg 905	Arg	Arg	Leu	Ser	Ile	Ile	Phe	
Ser	Asn	Asn 915	Asn	Met	Ile	Ser	Ser 920	Gln	Gly	Asn	Asn 925	Arg	Cys	Cys	Cys	
Cys	Cys 930	Ser	Asp	Gln	Gln	Arg 935	Gly	Gly	Thr	Asn	Thr 940	Thr	Lys	Arg	Gly	
Gly 945	Gly	Leu	Leu	Gly 950	Glu	Gly	Gly	Gly	Gly	Gly 955	Lys	Glu	Glu	Met	Cys 960	
Gly	Gly	Gly	Ile 965	Thr	Thr	Cys	Gln	Gln	Val 970	Gln	Thr	Thr	Leu	Ile	Gly 975	
Asn	Cys	Cys	His 980	Ser	Ser	Ser	Ala	Leu 985	Leu	Ala	Thr	Thr	Asn	Ala	Asn	
Asn	Gly 995	Gly	Gly	Gly	Lys	His	Leu 1000	Leu	Leu	Leu	Pro	Pro	Thr	Ile	Gly	
Gly	Arg 1010	Glu	Arg	Arg	Gly 1015	Gly	Gly	Gly	Gly	Ser	Ser	Ser	Ser	Ser	Asn	
Val 1025	Val	Phe	Lys	Lys	Ala 1030	Leu	Ile	Ile	Val	Leu	Leu	Ser	Ser	Leu	Thr 104	
Leu	Leu	Leu	Leu	Lys 1045	Gly	Pro	Pro	Lys	Ile	Phe	Phe	Leu	Leu	Leu	Gly 1055	
Lys	Gly	Gly	Ile 1060	Glu	Lys	Lys	Phe	Trp 1065	Trp	Trp	Trp	Trp	Lys	Arg	Phe	

Phe	Gly	Met	Met	Leu	Ser	Asn	Asn	His	Leu	Arg	Ala	Ala	Asn	Asp	Asn
		1075					1080					1085			
Asn	Asn	Asn	Asn	Ile	Pro	Pro	Arg	Phe	Ser	Ser	Thr	Ser	Ser	Lys	Asp
		1090				1095					1100				
Asp	Trp	Ile	Leu	Ala	Ala	Ala	Ala	His	Cys	Leu	Leu	Pro	Thr	Glu	Glu
1105					1110					1115					112
Glu	Ser	Ala	Ala	Ser	Ala	Phe	Phe	Lys	Arg	Arg	Arg	Arg	Arg	His	Gly
				1125					1130					1135	
Asn	Asn	Ile	Ile	Lys	Thr	Val	Val	Arg	Cys	Phe	Phe	Val	Lys	Lys	Gly
			1140					1145					1150		
Leu	Leu	Leu	Leu	Leu	Leu	Ala	Leu	Leu	Ser	Tyr	Gly	Gly	Glu	Lys	Lys
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Lys	Asp	Gln	Gln	Ala	Phe	Arg	Arg	Lys	Ser	Lys	Lys	Lys	Lys	Pro	Ile
	1170					1175					1180				
Leu	Leu	Gly	Phe	Glu	Glu	Ile	His	His	Lys	Leu	Leu	Gly	Ile	Glu	Glu
1185					1190					1195					120
Cys	Arg	Arg	Arg	Arg	Arg	Phe	His	Gln	Gln	Thr	Gly	Gly	Gly	Lys	Gln
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Gln	Leu	Glu	Phe	Phe	Leu	Pro	Pro	Asn	Phe	Val	Val	Val	Val	Val	Gly
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Gly	Gly	Glu	Ser	Ser	Ser	Leu	Ile	Lys	Lys	Gly	Ser	Ser	Leu	Cys	Cys
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Lys	Thr	Tyr	Tyr	Tyr	Tyr	Arg	Thr	Ser	Ser	Asp	Lys	Thr	Thr	Phe	Trp
	1250					1255					1260				
Trp	Ile	Phe	Gln	Met	Ile	Ile	Thr	Ser	Ser	Ser	Ser	Ser	Leu	Asn	Gln
1265					1270					1275					128
Gln	Asn	Ser	Ser	Ser	Trp	Leu	Leu	Ser	Ala	Gly	Gly	Ala	Ala	Leu	Val
				1285					1290					1295	
Asn	Asn	Asn	Asn	Asn	Ala	Leu	Leu	His	His	His	Thr	Leu	Val	Val	Glu
			1300					1305					1310		
Leu	Leu	His	His	His	Leu	Ala	Val	Lys	Lys	Lys	Leu	Asn	Asp	Asp	Ile
		1315				1320					1325				
Arg	Arg	Met	Ala	Asn	Lys	Ile	Ile	Glu	Gln	Gln	Gln	Gln	Gln	Ser	Leu
	1330					1335					1340				
Arg	Arg	Lys	Asn	Lys	Ile	Ile	Cys	Ala	Leu	Leu	Gly	Val	Tyr	Tyr	Tyr
1345					1350					1355					136
Tyr	Tyr	Gln	Gly	Gly	Arg	Leu	His	His	Cys	Leu	Asn	Asn	Leu	Gln	Gln
				1365					1370					1375	
Ile	Glu	Glu	Asn	Trp	Ala	Ala	Ala	Ala	Trp	Ala	Leu	Leu	Leu	Gly	Ser
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Ser	Gly	Val	Val	Thr	Ile	Phe	Phe	Gln	Arg	Gly	Gly	Phe	Gln	Gln	Gln
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Gln	Gln	Cys	Gly	Ile	Ile	Ile	Phe	Thr	Asn	Asn	Gln	Leu	Val	Val	Val
	1410														

	1540		1545		1550
Phe Cys Asn	Leu Met Met Leu	Val Asp Asp Phe	Lys Ser Ser Tyr	Lys	
	1555		1560		1565
Lys Thr Thr	Ile Ile Ile Ile	Ile Thr Leu Leu	Phe Arg Ala Ala	Thr	
	1570		1575		1580
Leu Leu Leu	Lys Ala Ala Ser	Phe Asp Asp Ile	Thr Thr Thr Thr	Leu	
1585		1590		1595	160
Leu Thr Thr	Asn Ser Asn Asn	Gln Gly Gly Ile	Leu Ala Ala Asn	Leu	
	1605		1610		1615
Asn Asn Gly	Ser Gly Ser Ser	Ala Arg Arg Glu	Asn Gly Gly Glu	Cys	
	1620		1625		1630
Gly Gly Ala	Ile Ile Lys Ser	Glu Glu Glu Glu	Glu Ser Leu Leu	Leu	
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Ser Ser Thr	Ile Lys Lys Asn	Gln Gln Asp Tyr	Trp Leu Ala Ala	Ala	
	1650		1655		1660
Ala Ile Leu	Arg Arg Met Ser	Tyr Tyr Gln Ser	Ser Ser Leu Ser	Ser Phe	
1665		1670		1675	168
Asn Thr Thr	Thr Gln Gln Gln	Gln Gln Arg Arg	Leu Leu Arg Leu	Leu	
	1685		1690		1695
Asn Ala Lys	Lys His Ala Leu	Leu Val Met Met	Asn Gln Ile Ile	Ile	
	1700		1705		1710
Ile Ile Arg	Gly Gly Glu Leu	Glu Glu Ile Thr	Ser Ser Leu Tyr	Tyr	
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Pro His Leu	Thr Ala Ala Ala	Ala Asn Ala Cys	Cys Leu Asn Gly	Gly	
	1730		1735		1740
Phe Thr Thr	Ala Met Thr Thr	Gln Pro Val Val	Tyr Trp Gly Ser	Ser	
1745		1750		1755	176
Trp Phe Lys	Asp Asp Ser Gly	Ala Ala Trp Cys	Cys Ser Ser Ile	Ile	
	1765		1770		1775
Ile Ile Ile	Tyr Asp Asp Ser	Ser Ser Ser Ala	Ser Leu Leu Lys	Pro	
	1780		1785		1790
Pro Gly Tyr	Ser Ser Pro Leu	Val Val Val Val	Trp Ser Ile Ile	Ile	
	1795		1800		1805
Lys Tyr Tyr	Ser Arg Arg Val	Leu Val Val Asp	Ala Ile Ile Ile	Cys	
	1810		1815		1820
Cys Cys Cys	Cys Gln Phe Phe	Phe Cys Cys Leu	Asn Glu Glu Phe	Cys	
1825		1830		1835	184
Gly Gly Lys	Gly				

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gct atg att aat aga gcg acc tta cac aat tat tct gaa att gaa aaa	168
Met Ile Asn Arg Ala Thr Leu His Asn Tyr Ser Glu Ile Glu Lys	
1 5 10 15	
aag aat atc atg ctc agt gat agg gtc gtt gtc att aga agc ggc gat	216
Lys Asn Ile Met Leu Ser Asp Arg Val Val Val Ile Arg Ser Gly Asp	
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<211> 189
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106290" ET56660

65		70		75		80									
Arg	Leu	Lys	Glu	Ser	Leu	Ile	His	Phe	Ala	Ser	Lys	Asp	Ala	Leu	Asn
				85					90					95	
Ile	Gln	Gly	Leu	Gly	Asp	Lys	Val	Ile	Glu	Gln	Leu	Phe	Glu	Glu	Lys
			100					105					110		
Leu	Ile	Phe	Asn	Ala	Leu	Asp	Leu	Tyr	Ala	Leu	Lys	Leu	Glu	Asp	Leu
		115					120					125			
Met	Arg	Leu	Asp	Lys	Phe	Lys	Ile	Lys	Lys	Ala	Gln	Asn	Leu	Leu	Asp
	130					135				140					
Ala	Ile	Leu	Lys	Ser	Lys	Asn	Pro	Pro	Leu	Trp	Arg	Leu	Ile	Asn	Ala
145					150					155				160	
Leu	Gly	Ile	Glu	His	Ile	Gly	Lys	Gly	Ala	Ser	Lys	Thr	Leu	Ala	Lys
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Tyr	Gly	Leu	Asn	Val	Leu	Glu	Lys	Ser	Glu	Xaa	Ser	Phe			
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Met Arg Pro Gly Val Leu Gln Val Gly Ala Met Tyr Ala Asn Gly Val	
	5 10 15
ggg atc caa acc aac aga tta aaa gcc gct cgc tat tat gaa tgg gtt	152
Gly Ile Gln Thr Asn Arg Leu Lys Ala Ala Arg Tyr Tyr Glu Trp Val	
	20 25 30
gca gcg ggg gcg atg cga ccg ctt gcg cga atc tgg ctc aga tgt atg	200
Ala Ala Gly Ala Met Arg Pro Leu Ala Arg Ile Trp Leu Arg Cys Met	
	35 40 45 50
aaa aca aga aaa atg cgg att caa acg ata aag aaa acg ctt tgc aat	248
Lys Thr Arg Lys Met Arg Ile Gln Thr Ile Lys Lys Thr Leu Cys Asn	
	55 60 65
tgt atg cgg tgg ctt gtc aag ggg ggg ata tgc tcg cat gca ata att	296
Cys Met Arg Trp Leu Val Lys Gly Gly Ile Cys Ser His Ala Ile Ile	
	70 75 80
tgg ggt gga tgt ttg cta acg gaa gtg ggg tcc caa aag att att aca	344
Trp Gly Gly Cys Leu Leu Thr Glu Val Gly Ser Gln Lys Ile Ile Thr	
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Lys Arg	
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aat	403

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 35 40 45  
 Cys Met Lys Thr Arg Lys Met Arg Ile Gln Thr Ile Lys Lys Thr Leu  
 50 55 60  
 Cys Asn Cys Met Arg Trp Leu Val Lys Gly Gly Ile Cys Ser His Ala  
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 85 90 95  
 Ile Thr Lys Arg  
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 <212> DNA  
 <213> Helicobacter pylori

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 Lys Lys Ile Val Val Asp Pro Ile Thr Arg Ile Glu Gly His Leu Arg  
 5 10 15  
 att gaa gtg atc gta gat gat gat aac gtg atc act gat gcg ttt tct 152  
 Ile Glu Val Ile Val Asp Asp Asp Asn Val Ile Thr Asp Ala Phe Ser  
 20 25 30  
 tct tct acg ctt ttt agg ggg cta gaa acc att att aaa ggc aga gat 200  
 Ser Ser Thr Leu Phe Arg Gly Leu Glu Thr Ile Ile Lys Gly Arg Asp  
 35 40 45 50  
 cca cga gat gca ggc ttc atc gct caa agg att tgc ggg gta tgc act 248  
 Pro Arg Asp Ala Gly Phe Ile Ala Gln Arg Ile Cys Gly Val Cys Thr  
 55 60 65  
 tat tcg cat tat aag gcc ggt atc acg gcg gta gaa aac gct cta ggc 296  
 Tyr Ser His Tyr Lys Ala Gly Ile Thr Ala Val Glu Asn Ala Leu Gly  
 70 75 80  
 atc act ccc cca tta aac gcg caa ttg gtg cga tct ttg atg aac atg 344  
 Ile Thr Pro Pro Leu Asn Ala Gln Leu Val Arg Ser Leu Met Asn Met  
 85 90 95

gcg Ala	ctg Leu	ctt Leu	ttt Phe	cat His	gac Asp	cat His	gtg Val	gtg Val	cat His	ttc Phe	tat Tyr	act Thr	ttg Leu	cat His	ggg Gly	392
ctt Leu	gat Asp	tgg Trp	tgc Cys	gat Asp	atc Ile	atg Met	agc Ser	gct Ala	tta Leu	aaa Lys	gcc Ala	gat Asp	ccc Pro	att Ile	caa Gln	440
gcg Ala	gca Ala	aaa Lys	ctt Leu	tct Ser	ttc Phe	aaa Lys	tac Tyr	agc Ser	cct Pro	tac Tyr	cct Pro	att Ile	aat Asn	acc Thr	ggg Gly	488
gcc Ala	ggt Gly	gaa Glu	tta Leu	aaa Lys	gcg Ala	gtt Val	caa Gln	aaa Lys	cgc Arg	ttg Leu	agc Ser	gat Asp	ttc Phe	gct Ala	aaa Lys	536
agc Ser	gga Gly	tct Ser	ttg Leu	ggg Gly	cct Pro	ttc Phe	agt Ser	aac Asn	ggc Gly	tat Tyr	tac Tyr	ggg Gly	cat His	aaa Lys	act Thr	584
tat Tyr	cgt Arg	tta Leu	agt Ser	ccg Pro	gag Glu	caa Gln	aat Asn	tta Leu	atc Ile	gtc Val	tta Leu	agc Ser	cac His	tac Tyr	ctc Leu	632
aag Lys	ctt Leu	tta Leu	gaa Glu	atc Ile	caa Gln	agg Arg	gaa Glu	gcg Ala	gcg Ala	aaa Lys	atg Met	acc Thr	gct Ala	att Ile	ttt Phe	680
ggg Gly	gcc Ala	aaa Lys	cag Gln	cct Pro	cac His	cca Pro	caa Gln	agc Ser	cta Leu	acg Thr	gtg Val	ggg Gly	ggt Gly	gtt Val	acg Thr	728
agt Ser	gtt Val	atg Met	gat Asp	ata Ile	ttg Leu	gat Asp	ccg Pro	acg Thr	aga Arg	ttg Leu	gct Ala	gaa Glu	tgg Trp	aag Lys	agc Ser	776
aag Lys	ttt Phe	gaa Glu	gtg Val	gtg Val	gcc Ala	aat Asn	ttc Phe	atc Ile	aac Asn	cat His	gct Ala	tac Tyr	tac Tyr	cct Pro	gat Asp	824
ttg Leu	gtg Val	atg Met	gca Ala	ggc Gly	gaa Glu	atg Met	ttc Phe	gct Ala	aac Asn	gaa Glu	caa Gln	tcc Ser	gtt Val	atc Ile	aaa Lys	872
ggc Gly	tgt Cys	ggc Gly	tta Leu	agg Arg	aat Asn	ttt Phe	atc Ile	gct Ala	tat Tyr	gaa Glu	gaa Glu	gtg Val	ctg Leu	ctt Leu	ggg Gly	920
agg Arg	gat Asp	aaa Lys	tac Tyr	ctt Leu	ttg Leu	agt Ser	agt Ser	ggg Gly	gtg Val	gtg Val	ctt Leu	gat Asp	ggg Gly	gat Asp	att Ile	968
tct Ser	aaa Lys	tta Leu	cac His	ccc Pro	att Ile	gat Asp	gaa Glu	agt Ser	ttg Leu	att Ile	aaa Lys	gaa Glu	gaa Glu	gtt Val	acg Thr	1016
cat His	tct Ser	tgg Trp	tat Tyr	caa Gln	tac Tyr	gaa Glu	gac Asp	act Thr	aaa Lys	gaa Glu	gtg Val	caa Gln	ctc Leu	cac His	cct Pro	1064



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gcg tta gtg gaa aat cta aaa agc gat caa agc act tgt gct cct tat Ala Leu Val Glu Asn Leu Lys Ser Asp Gln Ser Thr Cys Ala Pro Tyr 455 460 465	1448
cac att gat aaa aat caa gaa tat aaa ggg cgc tac att ggt caa gtg His Ile Asp Lys Asn Gln Glu Tyr Lys Gly Arg Tyr Ile Gly Gln Val 470 475 480	1496
cca agg ggc atg cta agc cat tgg gtg cgt att aaa aac ggc gtg gtg Pro Arg Gly Met Leu Ser His Trp Val Arg Ile Lys Asn Gly Val Val 485 490 495	1544
gaa aat tat caa gcg gtg gtg cct tct act tgg aat gca ggg cct aga Glu Asn Tyr Gln Ala Val Val Pro Ser Thr Trp Asn Ala Gly Pro Arg 500 505 510	1592
gat tct caa aat caa agg ggg gct tat gaa atg agc ttg att ggc act Asp Ser Gln Asn Gln Arg Gly Ala Tyr Glu Met Ser Leu Ile Gly Thr 515 520 525 530	1640
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tct ttt gac cca tgc atc gca tgc tcg gtg cat gtg atg gat ttt aaa Ser Phe Asp Pro Cys Ile Ala Cys Ser Val His Val Met Asp Phe Lys 550 555 560	1736
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565

570

575

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1837

&lt;210&gt; 18

&lt;211&gt; 578

&lt;212&gt; PRT

&lt;213&gt; Helicobacter pylori

&lt;400&gt; 18

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Lys	Thr	Tyr	Arg	Leu	Ser	Pro	Glu	Gln	Asn	Leu	Ile	Val	Leu	Ser	His
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Tyr	Leu	Lys	Leu	Leu	Glu	Ile	Gln	Arg	Glu	Ala	Ala	Lys	Met	Thr	Ala
		195					200					205			
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Val	Thr	Ser	Val	Met	Asp	Ile	Leu	Asp	Pro	Thr	Arg	Leu	Ala	Glu	Trp
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Pro	Asp	Leu	Val	Met	Ala	Gly	Glu	Met	Phe	Ala	Asn	Glu	Gln	Ser	Val
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Asp	Ile	Ser	Lys	Leu	His	Pro	Ile	Asp	Glu	Ser	Leu	Ile	Lys	Glu	Glu
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His	Pro	Tyr	Asp	Gly	Gln	Thr	Asn	Pro	His	Tyr	Thr	Gly	Leu	Lys	Asp
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Gly	Glu	Ser	Val	Gly	Ile	Glu	Asn	Lys	Ile	Ile	Pro	Ala	Lys	Val	Leu
		355					360					365			
Asp	Thr	Lys	Asn	Lys	Tyr	Ser	Trp	Ile	Lys	Ser	Pro	Arg	Tyr	Asp	Ser
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T05290"CT655501

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Thr Lys Leu Pro Leu Glu Ala Leu Phe Ser Thr Leu Gly Arg Thr Ala						
		420		425		430
Ala Arg Cys Ile Glu Ala Lys Thr Ile Ala Asp Asn Gly Leu Leu Ala						
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Phe Asp Ala Leu Val Glu Asn Leu Lys Ser Asp Gln Ser Thr Cys Ala						
		450		455		460
Pro Tyr His Ile Asp Lys Asn Gln Glu Tyr Lys Gly Arg Tyr Ile Gly						
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Gln Val Pro Arg Gly Met Leu Ser His Trp Val Arg Ile Lys Asn Gly						
		485		490		495
Val Val Glu Asn Tyr Gln Ala Val Val Pro Ser Thr Trp Asn Ala Gly						
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Pro Arg Asp Ser Gln Asn Gln Arg Gly Ala Tyr Glu Met Ser Leu Ile						
		515		520		525
Gly Thr Lys Ile Ala Asp Leu Thr Gln Pro Leu Glu Ile Ile Arg Thr						
		530		535		540
Ile His Ser Phe Asp Pro Cys Ile Ala Cys Ser Val His Val Met Asp						
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Lys Phe						

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Met Ser Gln Lys Ile Leu Ile Leu Gly Ile Gly	
1 5 10	
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Asn Ile Leu Phe Gly Asp Glu Gly Ile Gly Val His Leu Ala His Tyr	
15 20 25	
ctc aaa aaa aat ttt tct ttt ttc cct agc gtg gat att ata gat ggg	208
Leu Lys Lys Asn Phe Ser Phe Phe Pro Ser Val Asp Ile Ile Asp Gly	
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Gly Thr Met Ala Gln Gln Leu Ile Pro Leu Ile Thr Ser Tyr Glu Lys	
45 50 55	
gtt ttg att ttg gat tgc gtg agc gct gaa ggc gtt gag ata gga tca	304
Val Leu Ile Leu Asp Cys Val Ser Ala Glu Gly Val Glu Ile Gly Ser	
60 65 70 75	
gtc tat gct ttt gat ttt aag gac gct cct aaa gaa atc aca tgg gct	352
Val Tyr Ala Phe Asp Phe Lys Asp Ala Pro Lys Glu Ile Thr Trp Ala	

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80	85	90	
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Gly Ser Ala His 95	Leu His Thr 100	Leu Arg Leu Thr Glu 105	
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Phe Leu Gly Asp 110	Leu Pro Lys Thr Phe Ile Val 115	Gly Leu Val Pro Phe 120	
gtg ata ggg agc gag acc act ttc aag ctt tca agc aaa att tta aac			496
Val Ile Gly Ser Glu Thr 125	Thr Phe Lys Leu Ser 130	Ser Ser Lys Ile Leu Asn 135	
gct tta gaa acc gcc tta aaa gcc ata gaa acc caa ctc aac gca tgg			544
Ala Leu Glu Thr 140	Ala Leu Lys Ala Ile Glu Thr 145	Gln Leu Asn Ala Trp 150 155	
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Gly Val Lys Met 160	Gln Arg Thr Asp His Ile Ala Leu Glu Cys 165	Ile Ala 170	
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Glu Leu Ser Tyr Lys Gly Phe 175			
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Phe Lys Asp Ala Pro Lys Glu Ile Thr Trp Ala Gly Ser Ala His Glu			
85 90 95			
Val Glu Met Leu His Thr Leu Arg Leu Thr Glu Phe Leu Gly Asp Leu			
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Pro Lys Thr Phe Ile Val Gly Leu Val Pro Phe Val Ile Gly Ser Glu			
115 120 125			
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130 135 140			
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Gly Phe			

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**069471 - DEPT.**

**SECRET**

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tta Leu	aag Lys	gcc Ala	atg Met	acc Thr 135	gct Ala	gca Ala	gaa Glu	gtg Val	cat His 140	ttt Phe	tta Leu	agc Ser	gtt Val	aaa Lys 145	ttc Phe	488
aac Asn	aaa Lys	cct Pro	ttt Phe 150	gaa Glu	ttg Leu	gtg Val	cta Leu	gaa Glu 155	gac Asp	atg Met	ctc Leu	aaa Lys	gcc Ala 160	ggg Gly	gtg Val	536
gat Asp	tcc Ser	atg Met 165	cct Pro	ggg Gly	ggg Gly	ggg Gly	gcg Ala 170	gag Glu	att Ile	ttt Phe	gat Asp 175	gaa Glu	gaa Glu	atc Ile	agg Arg	584
cgt Arg	aaa Lys 180	atc Ile	tgt Cys	aat Asn	ggg Gly	aag Lys 185	gtg Val	gga Gly	tct Ser	tct Ser	cgg Arg 190	tgg Trp	tta Leu	gaa Glu	atc Ile	632
cat His 195	gct Ala	tat Tyr	tgg Trp	cac His 200	aaa Lys	tta Leu	ggc Gly	aaa Lys	atg Met	agt Ser 205	aac Asn	gct Ala	acc Thr	atg Met	ctt Leu 210	680
ttt Phe	ggg Gly	cat His	att Ile 215	gaa Glu	aat Asn	aaa Lys	atc Ile	cat His	cgc Arg 220	atc Ile	gat Asp	cac His	atg Met	cta Leu 225	aga Arg	728
atc Ile	aaa Lys	aaa Lys	atc Ile 230	caa Gln	agc Ser	cct Pro	aaa Lys	aat Asn 235	caa Gln	gta Val	gaa Glu	aac Asn	aaa Lys 240	gaa Glu	ggg Gly	776
ggg Gly	ttt Phe	aac Asn 245	gct Ala	ttt Phe	atc Ile	ccc Pro	ttg Leu 250	ttg Leu	tat Tyr	caa Gln	aaa Lys	gaa Glu 255	aac Asn	aat Asn	tat Tyr	824
ttg Leu	aat Asn 260	gtg Val	gaa Glu	aaa Lys	tcc Ser	ccc Pro 265	agt Ser	gcg Ala	ata Ile	gaa Glu	atc Ile 270	tta Leu	aaa Lys	acc Thr	atc Ile	872
gcc Ala 275	ata Ile	tct Ser	cgc Arg	att Ile 280	ctt Leu	tta Leu	aac Asn	aat Asn	atc Ile	cct Pro 285	cac His	att Ile	aaa Lys	gct Ala	tat Tyr 290	920
tgg Trp	gcg Ala	act Thr	ttg Leu 295	ggc Gly	ttg Leu	aat Asn	ttg Leu	gct Ala	tta Leu 300	gtg Val	gct Ala	caa Gln	gaa Glu	ttt Phe 305	ggc Gly	968
gct Ala	aac Asn	gat Asp 310	tta Leu	gac Asp	ggc Gly	acg Thr	ata Ile	gag Glu 315	ata Ile	gag Glu	agc Ser	att Ile	caa Gln 320	agc Ser	gcg Ala	1016
gca Ala	ggc Gly	gca Ala 325	aag Lys	agc Ser	cgg Arg	cat His	ggg Gly 330	tta Leu	gaa Glu	aaa Lys	gaa Glu	gat Asp 335	ttg Leu	ata Ile	ttt Phe	1064
aaa Lys	atc Ile	aag Lys	gac Asp	gct Ala	ggg Gly	ttt Phe	gtt Val	gcg Ala	gta Val	gaa Glu	agg Arg	gat Asp	agt Ser	ttg Leu	tat Tyr	1112

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Ala	Asp	Arg	Met	Arg	Gln	Asn	Met 40	His	Gln	Lys	Ile	Val 45	Tyr	Phe	Asn
Val	Asn 50	Arg	His	Leu	Asn	Pro 55	Ser	Asn	Ile	Cys	Ala 60	Asp	Ala	Cys	Lys
Phe 65	Cys	Ala	Phe	Ser	Ala 70	His	Arg	Lys	Asn	Pro 75	Asn	Pro	Tyr	Glu	Met 80
Ser	Leu	Glu	Glu	Ile 85	Leu	Glu	Lys	Val	Lys 90	Asn	Ser	Tyr	Asn	Lys 95	Gly
Ile	Lys	Glu	Val 100	His	Ile	Val	Ser	Ala 105	His	Asn	Pro	Asn	Tyr 110	Ser	Tyr
Glu	Trp	Tyr 115	Leu	Lys	Val	Phe	Glu 120	Thr	Ile	Lys	Gln	Glu 125	Met	Pro	Asn
Leu	His 130	Leu	Lys	Ala	Met	Thr 135	Ala	Ala	Glu	Val	His 140	Phe	Leu	Ser	Val
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Gly	Val	Asp	Ser	Met 165	Pro	Gly	Gly	Gly	Ala 170	Glu	Ile	Phe	Asp	Glu 175	Glu
Ile	Arg	Arg	Lys 180	Ile	Cys	Asn	Gly	Lys 185	Val	Gly	Ser	Ser	Arg 190	Trp	Leu
Glu	Ile 195	His	Ala	Tyr	Trp	His 200	Lys	Leu	Gly	Lys	Met 205	Ser	Asn	Ala	Thr
Met 210	Leu	Phe	Gly	His	Ile	Glu 215	Asn	Lys	Ile	His 220	Arg	Ile	Asp	His	Met
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Glu	Gly	Gly	Phe	Asn 245	Ala	Phe	Ile	Pro	Leu 250	Leu	Tyr	Gln	Lys	Glu 255	Asn
Asn	Tyr	Leu	Asn 260	Val	Glu	Lys	Ser	Pro 265	Ser	Ala	Ile	Glu	Ile 270	Leu	Lys
Thr	Ile 275	Ala	Ile	Ser	Arg	Ile 280	Leu	Leu	Asn	Asn	Ile 285	Pro	His	Ile	Lys
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Phe 305	Gly	Ala	Asn	Asp	Leu 310	Asp	Gly	Thr	Ile	Glu 315	Ile	Glu	Ser	Ile	Gln 320
Ser	Ala	Ala	Gly	Ala 325	Lys	Ser	Arg	His	Gly 330	Leu	Glu	Lys	Glu	Asp 335	Leu
Ile	Phe	Lys	Ile 340	Lys	Asp	Ala	Gly	Phe 345	Val	Ala	Val	Glu	Arg 350	Asp	Ser
Leu	Tyr	Asn	Phe	Ile	Gln	Lys	Phe								

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Lys Leu Pro Lys Lys Arg Val Ser Lys Thr Lys Ser Gln Lys Leu Ile		
5	10 15	
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His Ser Leu Thr Thr Gln Lys Asn Arg Ala Phe Leu Lys Lys Ile Ser		
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Ala Asn Glu Met Leu Leu Glu Leu Glu Lys Gly Ala Phe Lys Lys Asn		
35	40 45 50	
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Glu Ala Tyr Phe Ile Ser Asp Glu Glu Asp Lys Asn Tyr Val Leu Val		
55	60 65	
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Pro Asp Asn Val Ile Ser Leu Leu Ala Glu Asn Ala Arg Lys Ala Phe		
70	75 80	
gaa gcc agg ctt agg gcg gaa tta gaa agg gat att atc acc caa gcg		344
Glu Ala Arg Leu Arg Ala Glu Leu Glu Arg Asp Ile Ile Thr Gln Ala		
85	90 95	
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Pro Ile Asp Phe Glu Asp Val Arg Glu Val Ser Leu Gln Leu Leu Glu		
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Asn Leu Arg Gln Lys Asp Gly Asn Leu Pro Asn Ile Asn Thr Leu Asn		
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135	140 145	
gac aac atg ttc aaa caa ccc cct ttt aat gag aat aat ttt gaa aat		536
Asp Asn Met Phe Lys Gln Pro Pro Phe Asn Glu Asn Asn Phe Glu Asn		
150	155 160	
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Phe Asp Asn Ser Asp Glu Glu Asn Phe		
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616

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 50 55 60  
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 65 70 75 80  
 Ala Phe Glu Ala Arg Leu Arg Ala Glu Leu Glu Arg Asp Ile Ile Thr  
 85 90 95  
 Gln Ala Pro Ile Asp Phe Glu Asp Val Arg Glu Val Ser Leu Gln Leu  
 100 105 110  
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 115 120 125  
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 5 10 15  
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 Lys Cys Ala Lys Cys Val Pro Gly Cys Thr Ile Tyr Arg Ile His Lys  
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 Asp Glu Ala Thr Ser Pro Arg Gly Phe Leu Asp Leu Met Arg Leu Asn  
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952

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aca Thr 20	caa Gln	aat Asn	gcg Ala	cga Arg	tgg Trp 25	ata Ile	gat Asp	caa Gln	aaa Lys	tgc Cys 30	acc Thr	cct Pro	gat Asp	gtg Val	ttg Leu 35	153
tct Ser	ctt Leu	gtt Val	gct Ala	gat Asp 40	tgt Cys	att Ile	tta Leu	gag Glu	ttt Phe 45	acg Thr	caa Gln	tgt Cys	aat Asn	att Ile 50	gga Gly	201
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tat Tyr 100	agc Ser	ggg Gly	att Ile	tta Leu	ttt Phe 105	gaa Glu	aca Thr	aaa Lys	act Thr	ggc Gly 110	aat Asn	aga Arg	aat Asn	att Ile	tat Tyr 115	393
acc Thr	ata Ile	caa Gln	aac Asn	ata Ile 120	gag Glu	cta Leu	tta Leu	gaa Glu	tat Tyr 125	ctc Leu	atg Met	caa Gln	aga Arg	gaa Glu 130	aca Thr	441
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agt Ser	ggg Gly 150	att Ile	tat Tyr	cct Pro	tta Leu	ttt Phe 155	gac Asp	aac Asn	ttt Phe	tta Leu	caa Gln	aaa Lys 160	caa Gln	gac Asp	aca Thr	537
gaa Glu 165	agt Ser	ttt Phe	aag Lys	caa Gln	cta Leu	aaa Lys 170	gat Asp	ggg Gly	ttc Phe	act Thr	cat His 175	ttt Phe	act Thr	atc Ile	aat Asn	585
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cgt Arg	atc Ile	aat Asn 230	tgg Trp	cga Arg	gat Asp	ata Ile	gga Gly 235	aaa Lys	gat Asp	aaa Lys	aat Asn	acc Thr 240	acc Thr	aga Arg	caa Gln	777

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 Glu Tyr Asp Leu Ile Asn Ser Lys Arg Ile Ala Asn Ser Asn Tyr Leu  
 245 250 255

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 Ile Ser Lys Ala Lys Lys Val Val Lys Arg Tyr Asn Asp Arg Phe Asn  
 260 265 270 275

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 Asn Ser Leu Ser Glu Val Lys Gln Glu Lys Glu Glu Ser Gln Ala Thr  
 280 285 290

caa ata cac cat att ttt ccc atc caa gac ttt ccc att att gct aac 969  
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 295 300 305

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 310 315 320

gcc cac cct aat aat caa acc cgc ttg att gat aaa gat ttt caa tat 1065  
 Ala His Pro Asn Asn Gln Thr Arg Leu Ile Asp Lys Asp Phe Gln Tyr  
 325 330 335

atc tgc tta tta gct aaa acg acc aca att ctt aat gac act caa ggc 1113  
 Ile Cys Leu Leu Ala Lys Thr Thr Thr Ile Leu Asn Asp Thr Gln Gly  
 340 345 350 355

gta tat gat tgg aat gat tat att gtt gtg ttg aat atg ggc ctc aaa 1161  
 Val Tyr Asp Trp Asn Asp Tyr Ile Val Val Leu Asn Met Gly Leu Lys  
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aca act atc ttt tct caa gtc aag aac gaa tgg gaa tta tta aaa gta 1209  
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 375 380 385

ata gat gct ttt tat ttt gat ttt aac aag agc aaa gat cca agt tgg 1257  
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 390 395 400

tca tac ttg cta gat aaa aac gat tta aga gct ttc aag cta aaa ttt 1305  
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 Asp Val Leu Ser Leu Val Ala Asp Cys Ile Leu Glu Phe Thr Gln Cys  
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65      70      75      80
Asp Phe Ser Met His Glu Tyr Asp Lys Phe Phe Ser Gln Pro Ile Lys
85      90      95
Leu Leu Ala Tyr Ser Gly Ile Leu Phe Glu Thr Lys Thr Gly Asn Arg
100     105     110
Asn Ile Tyr Thr Ile Gln Asn Ile Glu Leu Leu Glu Tyr Leu Met Gln
115     120     125
Arg Glu Thr Asn Ala Leu Lys Phe Leu Ile Leu Tyr Ile Gln Lys Val
130     135     140
Leu Met Asp Ser Gly Ile Tyr Pro Leu Phe Asp Asn Phe Leu Gln Lys
145     150     155     160
Gln Asp Thr Glu Ser Phe Lys Gln Leu Lys Asp Gly Phe Thr His Phe
165     170     175
Thr Ile Asn Asn Thr Ala Ile Asn Asn Ala Thr Glu Cys Phe Arg Ile
180     185     190
Phe Thr Lys Ile Ile Asn Pro Leu Ala Phe Tyr Tyr Gly Lys Lys Gly
195     200     205
Thr Arg Lys Gly Tyr Leu Ser Asn Thr Ile Ile Thr Lys Asp Glu Leu
210     215     220
Asn Tyr Asn Arg Ile Asn Trp Arg Asp Ile Gly Lys Asp Lys Asn Thr
225     230     235     240
Thr Arg Gln Glu Tyr Asp Leu Ile Asn Ser Lys Arg Ile Ala Asn Ser
245     250     255
Asn Tyr Leu Ile Ser Lys Ala Lys Lys Val Val Lys Arg Tyr Asn Asp
260     265     270
Arg Phe Asn Asn Ser Leu Ser Glu Val Lys Gln Glu Lys Glu Glu Ser
275     280     285
Gln Ala Thr Gln Ile His His Ile Phe Pro Ile Gln Asp Phe Pro Ile
290     295     300
Ile Ala Asn Tyr Ile Glu Asn Leu Ile Ala Leu Thr Pro Asn Gln His
305     310     315     320
Phe Ile Tyr Ala His Pro Asn Asn Gln Thr Arg Leu Ile Asp Lys Asp
325     330     335
Phe Gln Tyr Ile Cys Leu Leu Ala Lys Thr Thr Thr Ile Leu Asn Asp
340     345     350
Thr Gln Gly Val Tyr Asp Trp Asn Asp Tyr Ile Val Val Leu Asn Met
355     360     365
Gly Leu Lys Thr Thr Ile Phe Ser Gln Val Lys Asn Glu Trp Glu Leu
370     375     380
Leu Lys Val Ile Asp Ala Phe Tyr Phe Asp Phe Asn Lys Ser Lys Asp
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Ala Ile Arg Asp Thr Gly His Phe Leu Asp Cys Ser Phe Asp Ile His	
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Asp Ser Val Gly Val Leu Asp Glu Tyr Phe Ala Gln Ser Glu Phe Phe	
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Thr Asn Ile Glu Asp Phe Glu Lys His Leu Glu Gln Ser Lys Asp Met	
55 60 65	
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Gly Lys Glu Ile Asn Tyr Leu Ser Val Cys Thr Pro Thr His Thr His	
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Phe Asp His Ile Arg Phe Gly Leu Arg Asn Gly Met His Val Ile Cys	
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Glu Lys Pro Leu Val Leu Asp Pro Gly Glu Ile Gln Glu Leu Lys Asp	
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Leu Glu Val Lys His Gln Lys Arg Val Phe Ser Leu Leu Pro Leu Arg	
115 120 125 130	
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Ser Trp Gly Asn Gly Ala Trp Thr Leu Leu Gly Phe Ser Met Gln Met	
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Ala Leu Ile Leu Val Leu Gly Gln Ala Leu Ala Asn Ala Lys Leu Val	
70 75 80	
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Gln Lys Leu Leu Lys Tyr Leu Ala Ser Leu Pro Lys Gly Tyr Tyr Thr	
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Trp Gly Phe Gly Leu Val Ile Ser Ala Ile Phe Ala Lys Glu Ile Ala	
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Lys Asn Val Lys Gly Val Asp Tyr Arg Leu Leu Ile Ala Ser Ala Tyr	
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Ser Val Ala Thr Gln Asn Glu Asn Leu Ser Lys Ile Ser Ala Gly Val	
165 170 175	
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Ile Glu Lys Ala Ile Pro Ile Ser Gln Thr Ile Phe Ser Ser Tyr Asn	
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005591-06901

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Gln Met Ala Leu Ile Leu Val Leu Gly Gln Ala Leu Ala Asn Ala Lys			
Leu Val Gln Lys Leu Leu Lys Tyr Leu Ala Ser Leu Pro Lys Gly Tyr			
Tyr Thr Ala Leu Trp Leu Val Thr Phe Leu Ser Leu Ile Ala Asn Trp			
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Ala Glu Asn Ile Leu Ala Tyr Thr Phe Phe Gln Glu Gly Leu Met Glu	
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Ile Lys Thr His Ser Ser Asn Glu Lys Glu Arg Phe Val Arg Ile Glu																
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      50      55      60
Lys Glu Thr Ser Lys Asn Ala Lys Leu Ser Leu Trp Ile Phe Ile Gly
      65      70      75      80
Gly Val Val Ala Ile Val Phe Tyr Ala Ser Ala Ile Ser Lys Asn Ile
      85      90      95
Ala Phe Val Ser Pro Val Val Leu Gly Arg Asp His Ala Ile Val Ser
      100      105      110
Phe Met Leu Ser Val Ala Thr Leu Ile Val Leu Phe Cys Lys Ile Asn
      115      120      125
Ala Asn Glu Ile Ala His Ser Ser Val Phe Lys Ser Gly Met Gln Ala
      130      135      140
Cys Val Cys Val Leu Gly Val Ala Trp Leu Gly Asp Thr Phe Val Ser
      145      150      155      160
Asn His Ile Asp Glu Ile Lys Arg Tyr Ala Ser Phe Leu Ile Ala Asp
      165      170      175
Tyr Pro Phe Leu Leu Ala Val Ala Leu Phe Leu Ala Ser Met Leu Leu
      180      185      190
Tyr Ser Gln Ala Ala Thr Ser Lys Ala Leu Ile Pro Ser Val Ile Thr
      195      200      205
Ala Leu Gly Ile Ser Ala Asn His Thr Glu His Leu Tyr Ile Ile Val
      210      215      220
Ala Ser Phe Ala Ser Val Ser Ala Leu Phe Val Leu Pro Thr Tyr Pro
      225      230      235      240
Thr Leu Leu Gly Ala Ile Ala Met Asp Asn Thr Gly Thr Thr Lys Met
      245      250      255
Gly Arg Tyr Val Phe Asp His Ala Phe Leu Ile Pro Gly Val Leu Val
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Val Ser Leu Ser Val Ala Leu Gly Phe Val Val Ala Pro Leu Val Leu
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<400> 43

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Glu Asn Ser Ser Ile Trp Ser Asn Pro Ala Phe Val Ala Ile Ile Cys
      5      10      15

atg tgc gtt ctt agc ctt tta agg ctc aat gtc atg ctt tct atg att      152
Met Cys Val Leu Ser Leu Leu Arg Leu Asn Val Met Leu Ser Met Ile
      20      25      30

agt gcg act ctc ata gca gga ctt atg gga ggg ctt ggg atc acg gag      200
Ser Ala Thr Leu Ile Ala Gly Leu Met Gly Gly Leu Gly Ile Thr Glu

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Ser	Phe	Asn	Ala	Met	Ile	Asp	Gly	Met	Lys	Gly	Asn	Leu	Asn	Ile	Ala	
				55					60					65		
tta	agc	tac	atc	ctt	tta	ggg	gct	tta	gcg	gta	gcg	atc	gct	aaa	agc	296
Leu	Ser	Tyr	Ile	Leu	Leu	Gly	Ala	Leu	Ala	Val	Ala	Ile	Ala	Lys	Ser	
			70					75					80			
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Asn	Leu	Ile	Lys	Val	Ala	Leu	Ser	Lys	Leu	Ile	Gly	Leu	Met	Asp	Tyr	
		85					90					95				
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Lys	Arg	Ser	Thr	Phe	Cys	Phe	Leu	Ile	Ala	Phe	Ile	Ala	Cys	Phe	Ser	
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caa	aat	tta	gtg	ccg	gtg	cat	atc	gct	ttt	atc	cct	att	tta	atc	ccc	440
Gln	Asn	Leu	Val	Pro	Val	His	Ile	Ala	Phe	Ile	Pro	Ile	Leu	Ile	Pro	
115				120						125					130	
cct	ctt	ttg	cat	tta	atg	aac	cgg	cta	gaa	ttg	gat	aga	aga	gcg	gtc	488
Pro	Leu	Leu	His	Leu	Met	Asn	Arg	Leu	Glu	Leu	Asp	Arg	Arg	Ala	Val	
				135					140					145		
gct	tgc	gct	tta	acc	ttt	ggc	ttg	caa	gcc	ccc	tac	ttg	gtg	ctt	cct	536
Ala	Cys	Ala	Leu	Thr	Phe	Gly	Leu	Gln	Ala	Pro	Tyr	Leu	Val	Leu	Pro	
			150					155					160			
gta	ggg	ttt	ggc	ttg	att	ttt	caa	acc	acc	att	tta	gag	caa	tta	aaa	584
Val	Gly	Phe	Gly	Leu	Ile	Phe	Gln	Thr	Thr	Ile	Leu	Glu	Gln	Leu	Lys	
		165					170					175				
gct	aat	ggc	gtt	agc	acc	acc	ata	gcg	caa	atc	aca	gga	gtg	atg	tgg	632
Ala	Asn	Gly	Val	Ser	Thr	Thr	Ile	Ala	Gln	Ile	Thr	Gly	Val	Met	Trp	
	180					185					190					
ata	gcg	ggg	tta	gcg	atg	gtc	gtt	gga	ctg	ctt	gtt	gct	gta	tta	acg	680
Ile	Ala	Gly	Leu	Ala	Met	Val	Val	Gly	Leu	Leu	Val	Ala	Val	Leu	Thr	
195				200						205					210	
cta	tac	aaa	aaa	ccc	agg	cac	tac	aaa	gag	aaa	tct	ttt	aat	ata	gaa	728
Leu	Tyr	Lys	Lys	Pro	Arg	His	Tyr	Lys	Glu	Lys	Ser	Phe	Asn	Ile	Glu	
				215					220					225		
aat	tac	gcc	tcg	ctt	caa	tta	aac	tac	cat	gac	tac	ttg	act	ttt	ata	776
Asn	Tyr	Ala	Ser	Leu	Gln	Leu	Asn	Tyr	His	Asp	Tyr	Leu	Thr	Phe	Ile	
			230					235					240			
ggg	att	gtc	gta	gcg	ttt	gtg	atc	caa	tta	gcc	acc	gat	tcg	atg	ccc	824
Gly	Ile	Val	Val	Ala	Phe	Val	Ile	Gln	Leu	Ala	Thr	Asp	Ser	Met	Pro	
		245					250					255				
tta	gcc	gcc														

Lys Phe Lys Glu Thr Asp Ser Leu Met Asp Asp Ser Val Lys Met Met	
275 280 285 290	
gcg ttt atc gct ttt gtg atg ttg gtg gct agc ggg ttt gga gaa gtg	968
Ala Phe Ile Ala Phe Val Met Leu Val Ala Ser Gly Phe Gly Glu Val	
295 300 305	
ttg caa aaa gtg cat gcg ata gag ggc tta gtg aat gcg att aca agc	1016
Leu Gln Lys Val His Ala Ile Glu Gly Leu Val Asn Ala Ile Thr Ser	
310 315 320	
gta gtc caa ggg aag ctt tta ggg gct ttt tta atg ctt gtt gta ggg	1064
Val Val Gln Gly Lys Leu Leu Gly Ala Phe Leu Met Leu Val Val Gly	
325 330 335	
ctt ttt atc act atg ggg ata ggg act tct ttt ggc act att cct atc	1112
Leu Phe Ile Thr Met Gly Ile Gly Thr Ser Phe Gly Thr Ile Pro Ile	
340 345 350	
atc gct gtg ttt tat gtc cct tta tgc gcg aaa tta ggt ttt agc gta	1160
Ile Ala Val Phe Tyr Val Pro Leu Cys Ala Lys Leu Gly Phe Ser Val	
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gaa tct acg att tta ctc atc gca tagccgcagc tttaggcgat gcaggctcac	1214
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Met Ile Ser Ala Thr Leu Ile Ala Gly Leu Met Gly Gly Leu Gly Ile	
35 40 45	
Thr Glu Ser Phe Asn Ala Met Ile Asp Gly Met Lys Gly Asn Leu Asn	
50 55 60	
Ile Ala Leu Ser Tyr Ile Leu Leu Gly Ala Leu Ala Val Ala Ile Ala	
65 70 75 80	
Lys Ser Asn Leu Ile Lys Val Ala Leu Ser Lys Leu Ile Gly Leu Met	
85 90 95	
Asp Tyr Lys Arg Ser Thr Phe Cys Phe Leu Ile Ala Phe Ile Ala Cys	
100 105 110	
Phe Ser Gln Asn Leu Val Pro Val His Ile Ala Phe Ile Pro Ile Leu	
115 120 125	
Ile Pro Pro Leu Leu His Leu Met Asn Arg Leu Glu Leu Asp Arg Arg	
130 135 140	
Ala Val Ala Cys Ala Leu Thr Phe Gly Leu Gln Ala Pro Tyr Leu Val	
145 150 155 160	
Leu Pro Val Gly Phe Gly Leu Ile Phe Gln Thr Thr Ile Leu Glu Gln	
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Leu Lys Ala Asn Gly Val Ser Thr Thr Ile Ala Gln Ile Thr Gly Val	
180 185 190	



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Leu	Phe	Val	Ala 20	Phe	Phe	Ser	Ile	Ile 25	Trp	Arg	Ile	Leu	Ala 30	Leu	Ile
Ser	Gly	Phe 35	Pro	Ser	Cys	Cys	Leu 40	Tyr	Ser	Ser	Leu	Thr 45	Ser	Cys	Leu
Val 50	Ile	Phe	Lys	Glu	Leu	Val 55	Tyr	Trp	Arg	Arg	Leu 60	Ile	Ala	Lys	Ser
Ile 65	Lys	Ala	Lys	Thr 70	Lys	Asn	Lys	Asn	Lys	Ser 75	Glu	Glu	Met	Ser 80	His
Asn	Ala	Leu	Phe 85	Leu	Asn	His	Asn	Asn	Trp 90	Pro	Cys	Lys	Phe	Lys 95	Arg
Ala	Ala	Trp	Phe 100	Asn	Ser	Pro	Lys	Asn 105	Lys	Glu	Lys	Met	Lys	Asn 110	Pro
Arg	Lys	Lys 115	Ala	Lys	Lys	Thr	Phe 120	Lys	Val	Ile	Lys	Leu 125	Pro	Ser	Arg
Ser	Phe 130	Phe	Lys	Glu	Lys	Arg 135	Phe	Leu	Thr	Pro	Leu 140	Ile	Gly	Leu	Ile
Leu 145	Glu	Asn	Leu	Gly 150	Ser	Met	Thr	Leu	Gly	Ala 155	Lys	Ser	Gln	Pro 160	Asn
Cys	Lys	Thr	Leu	Asp	Lys	Asn	Ala	Thr	Thr	Thr	Lys	Met	Ile	Lys	Ile

Gly Lys Ser Asn Lys Lys Val Ser Leu Ala Ser Trp Leu Asn Ser Ser  
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 Tyr Gln Lys Ile Tyr Thr His Lys Val Val Phe Ser Ser Leu Phe Phe  
 5 10 15

ttg ttg ttt ttg ttc aat gtg gaa act ttg ttg ctt tcg cat ttc agc 153  
 Leu Leu Phe Leu Phe Asn Val Glu Thr Leu Leu Leu Ser His Phe Ser  
 20 25 30 35

gat gat ttt tcg caa ttg ttt ttt ttg ttt gaa aac cat gtt tat gat 201  
 Asp Asp Phe Ser Gln Leu Phe Phe Leu Phe Glu Asn His Val Tyr Asp  
 40 45 50

ttc att gtc aaa tta gat tat ttg ggg cta ata ggc gtt tct tta att 249  
 Phe Ile Val Lys Leu Asp Tyr Leu Gly Leu Ile Gly Val Ser Leu Ile  
 55 60 65

tat ctg ctt gtg ctt att cta aag cct ttc acc ctc acg cgc caa aaa 297  
 Tyr Leu Leu Val Leu Ile Leu Lys Pro Phe Thr Leu Thr Arg Gln Lys  
 70 75 80

tgc gct tgc gta ggg ata tta tgc ctt tct ttc tac gct tgg aat ttt 345  
 Cys Ala Cys Val Gly Ile Leu Cys Leu Ser Phe Tyr Ala Trp Asn Phe  
 85 90 95

cct gtt aaa gat tct tta atg gtg ctt tat ctt ttc tat ttt gcg ctg 393  
 Pro Val Lys Asp Ser Leu Met Val Leu Tyr Leu Phe Tyr Phe Ala Leu  
 100 105 110 115

tta gcg act tta ttg tgg cgt ttt tta ggg gct agc atg aag caa tct 441  
 Leu Ala Thr Leu Leu Trp Arg Phe Leu Gly Ala Ser Met Lys Gln Ser  
 120 125 130

ttc ttg ccc tct atg aat att tgc atc gtg tgg gtt ttt gct tct tct 489  
 Phe Leu Pro Ser Met Asn Ile Cys Ile Val Trp Val Phe Ala Ser Ser  
 135 140 145

tta cag agt ttt agg ttt tta agc gtg tct gat tgc gtg gat ttt tcc 537  
 Leu Gln Ser Phe Arg Phe Leu Ser Val Ser Asp Cys Val Asp Phe Ser  
 150 155 160

ctt ttt aca ctc gcg ctt att tta ttg ata ctg gtt tta atc tat tgc 585



Leu	Phe	Thr	Leu	Ala	Leu	Ile	Leu	Ile	Leu	Val	Leu	Ile	Tyr	Cys		
165						170				175						
aaa	cgc	ctt	ttt	ggg	ttg	tat	gaa	tac	gct	aac	acg	ctc	att	ttg	atc	633
Lys	Arg	Leu	Phe	Gly	Leu	Tyr	Glu	Tyr	Ala	Asn	Thr	Leu	Ile	Leu	Ile	
180					185					190					195	
gtg	ggg	ctt	agc	gtg	gtg	gtg	cta	tgc	tct	agc	atg	ttc	att	caa	act	681
Val	Gly	Leu	Ser	Val	Val	Val	Leu	Cys	Ser	Ser	Met	Phe	Ile	Gln	Thr	
				200					205					210		
aaa	gaa	tac	tat	ggc	atg	cga	ttg	ggg	ttt	tat	ttt	tta	ggc	ctg	tta	729
Lys	Glu	Tyr	Tyr	Gly	Met	Arg	Leu	Gly	Phe	Tyr	Phe	Leu	Gly	Leu	Leu	
			215					220					225			
ggg	tgg	ctt	tta	gaa	tat	gtg	cat	aac	act	tta	agg	cgt	ttg	gaa	cat	777
Gly	Trp	Leu	Leu	Glu	Tyr	Val	His	Asn	Thr	Leu	Arg	Arg	Leu	Glu	His	
		230				235						240				
caa	att	taa	agctcaa	ataggaatag	ctaaagcctt	ttgattgagt	gttttttttag									833
Gln	Ile															
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1				5					10					15		
Leu	Phe	Phe	Leu	Leu	Phe	Leu	Phe	Asn	Val	Glu	Thr	Leu	Leu	Leu	Ser	
			20					25					30			
His	Phe	Ser	Asp	Asp	Phe	Ser	Gln	Leu	Phe	Phe	Leu	Phe	Glu	Asn	His	
		35					40					45				
Val	Tyr	Asp	Phe	Ile	Val	Lys	Leu	Asp	Tyr	Leu	Gly	Leu	Ile	Gly	Val	
	50				55						60					
Ser	Leu	Ile	Tyr	Leu	Leu	Val	Leu	Ile	Leu	Lys	Pro	Phe	Thr	Leu	Thr	
65					70					75					80	
Arg	Gln	Lys	Cys	Ala	Cys	Val	Gly	Ile	Leu	Cys	Leu	Ser	Phe	Tyr	Ala	
				85					90					95		
Trp	Asn	Phe	Pro	Val	Lys	Asp	Ser	Leu	Met	Val	Leu	Tyr	Leu	Phe	Tyr	
			100					105					110			
Phe	Ala	Leu	Leu	Ala	Thr	Leu	Leu	Trp	Arg	Phe	Leu	Gly	Ala	Ser	Met	
		115					120					125				
Lys	Gln	Ser	Phe	Leu	Pro	Ser	Met	Asn	Ile	Cys	Ile	Val	Trp	Val	Phe	
	130					135					140					

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 225 230 235 240  
 Leu Glu His Gln Ile  
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 Met Leu Pro Phe Asp Val Phe  
 1 5

atc aaa tcc tac ccc acc cct tgt tat ttc aaa caa ttc tta cgg ctt 163  
 Ile Lys Ser Tyr Pro Thr Pro Cys Tyr Phe Lys Gln Phe Leu Arg Leu  
 10 15 20

aaa aaa acc tac ccc tcc aaa ctc aat gag agt ttt tta ttc agg cgt 211  
 Lys Lys Thr Tyr Pro Ser Lys Leu Asn Glu Ser Phe Leu Phe Arg Arg  
 25 30 35

att gat gcg ggg ttt att tct tct atc gcc ggc tat cca ttc gct ctt 259  
 Ile Asp Ala Gly Phe Ile Ser Ser Ile Ala Gly Tyr Pro Phe Ala Leu  
 40 45 50 55

cat tcc cat tct cta ggc att gtc gct tat aag gaa gtt tta agc gtg 307  
 His Ser His Ser Leu Gly Ile Val Ala Tyr Lys Glu Val Leu Ser Val  
 60 65 70

ctg gtt gtg gat aca aaa aac gct ttt gat aaa gaa agc gct tct tca 355  
 Leu Val Val Asp Thr Lys Asn Ala Phe Asp Lys Glu Ser Ala Ser Ser  
 75 80 85

aac gcc ctc tct caa gcg cta ggg tta aag ggc gaa gtg tta atc ggc 403  
 Asn Ala Leu Ser Gln Ala Leu Gly Leu Lys Gly Glu Val Leu Ile Gly  
 90 95 100

aat aaa gca ctg cag ttt tat tat tcc aac cct aaa aaa gat ttt ata 451  
 Asn Lys Ala Leu Gln Phe Tyr Tyr Ser Asn Pro Lys Lys Asp Phe Ile  
 105 110 115

gat tta gcc gct ctt tgg tat gaa aaa aaa cgc ttg ccg ttt gtt ttt 499  
 Asp Leu Ala Ala Leu Trp Tyr Glu Lys Lys Arg Leu Pro Phe Val Phe  
 120 125 130 135

ggg cgt ttg tgt tat tac caa aac aag gat ttt tac aag cgc ttg tct 547  
 Gly Arg Leu Cys Tyr Tyr Gln Asn Lys Asp Phe Tyr Lys Arg Leu Ser  
 140 145 150

tta gct ttc aaa cat caa aaa aca aaa atc cct tac tac atc ctt aaa 595  
 Leu Ala Phe Lys His Gln Lys Thr Lys Ile Pro Tyr Tyr Ile Leu Lys  
 155 160 165

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 <212> PRT  
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 Leu Ser Gly Glu Ile Asn Asp Ser Val Ala Ser Ser Ile Val Ala Gln  
 35 40 45  
 Leu Leu Phe Leu Glu Ala Glu Asp Pro Glu Lys Asp Ile Gly Leu Tyr  
 50 55 60  
 Ile Asn Ser Pro Gly Gly Val Ile Thr Ser Gly Leu Ser Ile Tyr Asp  
 65 70 75 80  
 Thr Met Asn Phe Ile Arg Pro Asp Val Ser Thr Ile Cys Ile Gly Gln  
 85 90 95  
 Ala Ala Ser Met Gly Ala Phe Leu Leu Ser Cys Gly Ala Lys Gly Lys  
 100 105 110  
 Arg Phe Ser Leu Pro His Ser Arg Ile Met Ile His Gln Pro Leu Gly  
 115 120 125  
 Gly Ala Gln Gly Gln Ala Ser Asp Ile Glu Ile Ile Ser Asn Glu Ile  
 130 135 140  
 Leu Arg Leu Lys Gly Leu Met Asn Ser Ile Leu Ala Gln Asn Ser Gly  
 145 150 155 160  
 Gln Ser Leu Glu Gln Ile Ala Lys Asp Thr Asp Arg Asp Phe Tyr Met  
 165 170 175  
 Ser Ala Lys Glu Ala Lys Glu Tyr Gly Leu Ile Asp Lys Val Leu Gln  
 180 185 190  
 Lys Asn Val Lys  
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 Arg Ile Lys Lys Glu Arg Leu Asn Lys Leu Leu Lys Arg Gly Phe Leu  
 1 5 10 15  
 gcg ttc ttt ttg agc gtg tat tta agg gct gat gat ttg gtt act tac 96  
 Ala Phe Phe Leu Ser Val Tyr Leu Arg Ala Asp Asp Leu Val Thr Tyr  
 20 25 30  
 acc atc atc aaa gaa aaa gat cta gga tac cag cgg ttt tta gcc aag 144  
 Thr Ile Ile Lys Glu Lys Asp Leu Gly Tyr Gln Arg Phe Leu Ala Lys  
 35 40 45  
 aag tgt tta agg ggt aaa acc cac cct ccg tgt ttt act aag cct aaa 192  
 Lys Cys Leu Arg Gly Lys Thr His Pro Pro Cys Phe Thr Lys Pro Lys  
 50 55 60

aag cct aaa aga aaa ctt ttt aat ata gac aaa agc tcc cac tat tat	240
Lys Pro Lys Arg Lys Leu Phe Asn Ile Asp Lys Ser Ser His Tyr Tyr	
65 70 75 80	
ggc aca agc gtg gtg caa atg tca tgg cta cag agt agg gaa aaa ttt	288
Gly Thr Ser Val Val Gln Met Ser Trp Leu Gln Ser Arg Glu Lys Phe	
85 90 95	
gaa aac cat tca aaa tac cga gac att cct ttt gct gaa gtc agt ttg	336
Glu Asn His Ser Lys Tyr Arg Asp Ile Pro Phe Ala Glu Val Ser Leu	
100 105 110	
att tat ggc tat aaa caa ttt ttt cct aaa aaa gag cgc tac ggc ttc	384
Ile Tyr Gly Tyr Lys Gln Phe Phe Pro Lys Lys Glu Arg Tyr Gly Phe	
115 120 125	
cgt ttt tat gtc tct ttg gat tac gct tat ggg ttt ttt ctt aaa aat	432
Arg Phe Tyr Val Ser Leu Asp Tyr Ala Tyr Gly Phe Phe Leu Lys Asn	
130 135 140	
aag ggc gtg ttg ggc gat agt ttg agg gag agt tcg caa atc cct aaa	480
Lys Gly Val Leu Gly Asp Ser Leu Arg Glu Ser Ser Gln Ile Pro Lys	
145 150 155 160	
agc tat aga gaa aaa ttg caa aga aaa gag act ttt att aac gct att	528
Ser Tyr Arg Glu Lys Leu Gln Arg Lys Glu Thr Phe Ile Asn Ala Ile	
165 170 175	
ttt tat ggc gcg gga gct gac ttt tta tac aaa cgc gct ttt gga acg	576
Phe Tyr Gly Ala Gly Ala Asp Phe Leu Tyr Lys Arg Ala Phe Gly Thr	
180 185 190	
ctg att tta ggg atg aat ttc gtg gga gaa acc tgg ttt tat gaa aca	624
Leu Ile Leu Gly Met Asn Phe Val Gly Glu Thr Trp Phe Tyr Glu Thr	
195 200 205	
aag att ttt aaa aag tgg gct aaa gat cct ttg agc gtt tat cac cct	672
Lys Ile Phe Lys Lys Trp Ala Lys Asp Pro Leu Ser Val Tyr His Pro	
210 215 220	
tac atg ttt caa gtg atg ttg aat gtg ggg tat cgt tac cgc' ttt tca	720
Tyr Met Phe Gln Val Met Leu Asn Val Gly Tyr Arg Tyr Arg Phe Ser	
225 230 235 240	
agg tat aag aat tgg gcg ata gaa ttg ggt gcg cgc atc cct ttt tta	768
Arg Tyr Lys Asn Trp Ala Ile Glu Leu Gly Ala Arg Ile Pro Phe Leu	
245 250 255	
acc aat gat tat ttt aaa acc cct tta tac acc ctt cat ttc aag cgc	816
Thr Asn Asp Tyr Phe Lys Thr Pro Leu Tyr Thr Leu His Phe Lys Arg	
260 265 270	
aat att tct gtc tat ctc act tca act tat gac ttt tagtttttta	862
Asn Ile Ser Val Tyr Leu Thr Ser Thr Tyr Asp Phe	
275 280	
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<211> 284  
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 <213> Helicobacter pylori

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 Thr Ile Ile Lys Glu Lys Asp Leu Gly Tyr Gln Arg Phe Leu Ala Lys  
 35 40 45  
 Lys Cys Leu Arg Gly Lys Thr His Pro Pro Cys Phe Thr Lys Pro Lys  
 50 55 60  
 Lys Pro Lys Arg Lys Leu Phe Asn Ile Asp Lys Ser Ser His Tyr Tyr  
 65 70 75 80  
 Gly Thr Ser Val Val Gln Met Ser Trp Leu Gln Ser Arg Glu Lys Phe  
 85 90 95  
 Glu Asn His Ser Lys Tyr Arg Asp Ile Pro Phe Ala Glu Val Ser Leu  
 100 105 110  
 Ile Tyr Gly Tyr Lys Gln Phe Phe Pro Lys Lys Glu Arg Tyr Gly Phe  
 115 120 125  
 Arg Phe Tyr Val Ser Leu Asp Tyr Ala Tyr Gly Phe Phe Leu Lys Asn  
 130 135 140  
 Lys Gly Val Leu Gly Asp Ser Leu Arg Glu Ser Ser Gln Ile Pro Lys  
 145 150 155 160  
 Ser Tyr Arg Glu Lys Leu Gln Arg Lys Glu Thr Phe Ile Asn Ala Ile  
 165 170 175  
 Phe Tyr Gly Ala Gly Ala Asp Phe Leu Tyr Lys Arg Ala Phe Gly Thr  
 180 185 190  
 Leu Ile Leu Gly Met Asn Phe Val Gly Glu Thr Trp Phe Tyr Glu Thr  
 195 200 205  
 Lys Ile Phe Lys Lys Trp Ala Lys Asp Pro Leu Ser Val Tyr His Pro  
 210 215 220  
 Tyr Met Phe Gln Val Met Leu Asn Val Gly Tyr Arg Tyr Arg Phe Ser  
 225 230 235 240  
 Arg Tyr Lys Asn Trp Ala Ile Glu Leu Gly Ala Arg Ile Pro Phe Leu  
 245 250 255  
 Thr Asn Asp Tyr Phe Lys Thr Pro Leu Tyr Thr Leu His Phe Lys Arg  
 260 265 270  
 Asn Ile Ser Val Tyr Leu Thr Ser Thr Tyr Asp Phe  
 275 280

<210> 55  
 <211> 1172  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (75)...(1106)

<400> 55  
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 actagggaggt taga atg atc tta aaa cga gtt act gaa gct tta gaa gcg 110  
 Met Ile Leu Lys Arg Val Thr Glu Ala Leu Glu Ala  
 1 5 10  
 tat aaa aat ggc gaa atg ctc att gtt atg gac gat gaa gac aga gaa 158  
 Tyr Lys Asn Gly Glu Met Leu Ile Val Met Asp Asp Glu Asp Arg Glu

15				20				25								
aat	gag	ggg	gat	ttg	gtt	tta	gct	ggg	att	ttt	tct	acc	cct	gag	aaa	206
Asn	Glu	Gly	Asp	Leu	Val	Leu	Ala	Gly	Ile	Phe	Ser	Thr	Pro	Glu	Lys	
30				35				40								
atc	aat	ttc	atg	gcc	acg	cat	gct	agg	ggg	ttg	att	tgc	gtg	tct	ttg	254
Ile	Asn	Phe	Met	Ala	Thr	His	Ala	Arg	Gly	Leu	Ile	Cys	Val	Ser	Leu	
45				50				55				60				
acc	aaa	gat	tta	gcg	aaa	aaa	ttt	gaa	tta	ccc	cct	atg	gtt	agc	gtg	302
Thr	Lys	Asp	Leu	Ala	Lys	Lys	Phe	Glu	Leu	Pro	Pro	Met	Val	Ser	Val	
				65				70				75				
aat	gat	tct	aac	cat	gag	acc	gct	ttc	acg	gtt	tcc	att	gac	gct	aaa	350
Asn	Asp	Ser	Asn	His	Glu	Thr	Ala	Phe	Thr	Val	Ser	Ile	Asp	Ala	Lys	
80								85				90				
gaa	gcc	aga	acc	ggg	att	tct	gct	ttt	gaa	agg	cat	tta	acg	att	gaa	398
Glu	Ala	Arg	Thr	Gly	Ile	Ser	Ala	Phe	Glu	Arg	His	Leu	Thr	Ile	Glu	
95				100				105								
tta	ttg	tgt	aaa	gac	acc	acc	aaa	ccg	agc	gat	ttt	gtg	cgc	ccg	ggg	446
Leu	Leu	Cys	Lys	Asp	Thr	Thr	Lys	Pro	Ser	Asp	Phe	Val	Arg	Pro	Gly	
110				115				120								
cat	att	ttc	cct	ttg	atc	gcc	aaa	gac	ggg	ggc	gtg	tta	gcg	cgc	acg	494
His	Ile	Phe	Pro	Leu	Ile	Ala	Lys	Asp	Gly	Gly	Val	Leu	Ala	Arg	Thr	
125				130				135				140				
ggc	cat	act	gaa	gcg	agc	gtg	gat	ttg	tgc	aaa	tta	gct	gga	tta	aag	542
Gly	His	Thr	Glu	Ala	Ser	Val	Asp	Leu	Cys	Lys	Leu	Ala	Gly	Leu	Lys	
				145				150				155				
ccc	gtg	agc	gtg	att	tgt	gaa	atc	atg	aaa	gaa	gat	ggc	tct	atg	gcg	590
Pro	Val	Ser	Val	Ile	Cys	Glu	Ile	Met	Lys	Glu	Asp	Gly	Ser	Met	Ala	
				160				165				170				
aga	agg	ggg	gat	aaa	ttt	ttg	agc	gat	ttc	gcc	ctc	aaa	cat	aac	ctt	638
Arg	Arg	Gly	Asp	Lys	Phe	Leu	Ser	Asp	Phe	Ala	Leu	Lys	His	Asn	Leu	
175				180				185								
aaa	act	ctc	tat	gtc	tct	gat	ttg	att	agc	tat	cgt	ttg	gaa	aat	gaa	686
Lys	Thr	Leu	Tyr	Val	Ser	Asp	Leu	Ile	Ser	Tyr	Arg	Leu	Glu	Asn	Glu	
190				195				200								
agt	ttg	ctg	aaa	atg	ttt	tgt	caa	gaa	gaa	agg	gaa	ttt	tta	aaa	cac	734
Ser	Leu	Leu	Lys	Met	Phe	Cys	Gln	Glu	Glu	Arg	Glu	Phe	Leu	Lys	His	
205				210				215				220				
caa	acg	caa	tgc	tac	act	ttt	tta	gat	cac	cag	caa	aaa	aac	cat	tac	782
Gln	Thr	Gln	Cys	Tyr	Thr	Phe	Leu	Asp	His	Gln	Gln	Lys	Asn	His	Tyr	
				225				230				235				
gct	ttt	aag	ttt	aaa	ggc	gca	aaa	acc	cat	gat	tta	gcc	cct	tta	gtg	830
Ala	Phe	Lys	Phe	Lys	Gly	Ala	Lys	Thr	His	Asp	Leu	Ala	Pro	Leu	Val	
				240				245				250				
cgt	ttc	cac	cct	atc	aaa	gag	gat	ttt	gat	ttt	tta	acg	act	gat	gcg	878





Tyr Thr Phe Leu Asp His Gln Gln Lys Asn His Tyr Ala Phe Lys Phe  
 225 230 235 240  
 Lys Gly Ala Lys Thr His Asp Leu Ala Pro Leu Val Arg Phe His Pro  
 245 250 255  
 Ile Lys Glu Asp Phe Asp Phe Leu Thr Thr Asp Ala Phe Glu Val Phe  
 260 265 270  
 Phe Lys Ala Leu Glu Tyr Leu Lys His Glu Gly Gly Tyr Leu Ile Phe  
 275 280 285  
 Met Asn Thr His Ser Lys Glu Asn Asn Val Val Lys Asp Phe Gly Ile  
 290 295 300  
 Gly Ala Leu Val Leu Lys Asn Leu Gly Ile Lys Asp Phe Arg Leu Leu  
 305 310 315 320  
 Ser Ser Cys Glu Asp Arg Gln Tyr Lys Ala Leu Ser Gly Phe Gly Leu  
 325 330 335  
 Lys Leu Val Glu Thr Ile Ser Leu  
 340

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 <211> 394  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (51)...(341)

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 Lys Leu  
 1  
 cat ttt aaa gcg ttt cac gca ctt ttc tat cct agc aat aga gac aat 104  
 His Phe Lys Ala Phe His Ala Leu Phe Tyr Pro Ser Asn Arg Asp Asn  
 5 10 15  
 atc tat gcc aat cat tta aaa tta ttg gat aat gaa atc agt gaa aaa 152  
 Ile Tyr Ala Asn His Leu Lys Leu Leu Asp Asn Glu Ile Ser Glu Lys  
 20 25 30  
 gac att ttt aat aaa gcc atc aat caa aaa cga att caa atg gct ctt 200  
 Asp Ile Phe Asn Lys Ala Ile Asn Gln Lys Arg Ile Gln Met Ala Leu  
 35 40 45 50  
 aat ctc atc ttt aag ctt gtt ttt gcc ttt gtt agt aac cac ttc ttc 248  
 Asn Leu Ile Phe Lys Leu Val Phe Ala Phe Val Ser Asn His Phe Phe  
 55 60 65  
 cac gct ttt aga cga cag aat ctc tat aat cgt gtc ttt aat cgc tgt 296  
 His Ala Phe Arg Arg Gln Asn Leu Tyr Asn Arg Val Phe Asn Arg Cys  
 70 75 80  
 gtc ttt aac ctt gac ttc att caa aag ctt ttc att act caa ttc 341  
 Val Phe Asn Leu Asp Phe Ile Gln Lys Leu Phe Ile Thr Gln Phe  
 85 90 95  
 taacgaaata gaagccttaa ggtagcgtct gccattttga gagaccagat tca 394

<210> 58  
 <211> 97

<212> PRT  
 <213> Helicobacter pylori

<400> 58  
 Lys Leu His Phe Lys Ala Phe His Ala Leu Phe Tyr Pro Ser Asn Arg  
 1 5 10 15  
 Asp Asn Ile Tyr Ala Asn His Leu Lys Leu Leu Asp Asn Glu Ile Ser  
 20 25 30  
 Glu Lys Asp Ile Phe Asn Lys Ala Ile Asn Gln Lys Arg Ile Gln Met  
 35 40 45  
 Ala Leu Asn Leu Ile Phe Lys Leu Val Phe Ala Phe Val Ser Asn His  
 50 55 60  
 Phe Phe His Ala Phe Arg Arg Gln Asn Leu Tyr Asn Arg Val Phe Asn  
 65 70 75 80  
 Arg Cys Val Phe Asn Leu Asp Phe Ile Gln Lys Leu Phe Ile Thr Gln  
 85 90 95  
 Phe

<210> 59  
 <211> 360  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (82)...(270)

<400> 59  
 acttaaaggc ataaaaacct taagcttttt gagtttcaaa agggtttcaa gctttttata 60  
 agactttttt tgaatgagta a gga gaa aat att ttg ttc cat aaa ctg atc 111  
 Gly Glu Asn Ile Leu Phe His Lys Leu Ile  
 1 5 10  
 tta aca tgc ttt tta gcg ctt gta gca ata acc att caa gct tgc ggt 159  
 Leu Thr Cys Phe Leu Ala Leu Val Ala Ile Thr Ile Gln Ala Cys Gly  
 15 20 25  
 tat aaa gcc cct cca ttc aat gaa aaa ccc gct aaa aaa act tca aac 207  
 Tyr Lys Ala Pro Pro Phe Asn Glu Lys Pro Ala Lys Lys Thr Ser Asn  
 30 35 40  
 agc tct aat tct tct atg caa acg ccc acc aac agc acc acg cca gaa 255  
 Ser Ser Asn Ser Ser Met Gln Thr Pro Thr Asn Ser Thr Thr Pro Glu  
 45 50 55  
 ttt tta aat cag cct taaaatcact gctcttggtt aagggttttg atttctaggg 310  
 Phe Leu Asn Gln Pro  
 60  
 tttttgtggc taacttttga nsttcgcttt catcatgcgt taccataatg 360

<210> 60  
 <211> 63  
 <212> PRT  
 <213> Helicobacter pylori

<400> 60  
 Gly Glu Asn Ile Leu Phe His Lys Leu Ile Leu Thr Cys Phe Leu Ala

1	5	10	15
Leu Val Ala	Ile Thr Ile Gln Ala Cys Gly Tyr Lys Ala Pro Pro Phe		
	20	25	30
Asn Glu Lys	Pro Ala Lys Lys Thr Ser Asn Ser Ser Asn Ser Ser Met		
	35	40	45
Gln Thr Pro	Thr Asn Ser Thr Thr Pro Glu Phe Leu Asn Gln Pro		
50	55	60	

<210> 61  
 <211> 445  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (51)...(392)

<400> 61  
 atttacaaag cgtgttggat accccaaga tgattcgttt ggaaaattga atg cgc 56  
 Met Arg  
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ttt ttg aac aac aaa cat aga gaa aag ggc tta aag gct gaa gaa gaa 104  
 Phe Leu Asn Asn Lys His Arg Glu Lys Gly Leu Lys Ala Glu Glu Glu  
 5 10 15

gct tgc gga ttt tta aaa tcg tta ggt ttt gaa atg gtg gag agg aac 152  
 Ala Cys Gly Phe Leu Lys Ser Leu Gly Phe Glu Met Val Glu Arg Asn  
 20 25 30

ttt ttt tca caa ttt ggc gaa att gat att atc gct ttg aaa aaa ggg 200  
 Phe Phe Ser Gln Phe Gly Glu Ile Asp Ile Ile Ala Leu Lys Lys Gly  
 35 40 45 50

gtt ttg cat ttc att gaa gtc aaa agc ggg gaa aat ttt gat ccc att 248  
 Val Leu His Phe Ile Glu Val Lys Ser Gly Glu Asn Phe Asp Pro Ile  
 55 60 65

tat gcg atc acg ccg agc aaa tta aaa aag atg att aaa acg atc cgc 296  
 Tyr Ala Ile Thr Pro Ser Lys Leu Lys Lys Met Ile Lys Thr Ile Arg  
 70 75 80

tgt tat ttg tcc caa aaa gat ccc aat agc gat ttt tgc ata gac gct 344  
 Cys Tyr Leu Ser Gln Lys Asp Pro Asn Ser Asp Phe Cys Ile Asp Ala  
 85 90 95

ctt att gtg aaa aat ggt aaa ttt gag ctt tta gaa aat atc act ttt 392  
 Leu Ile Val Lys Asn Gly Lys Phe Glu Leu Leu Glu Asn Ile Thr Phe  
 100 105 110

tagattttta cagaaagtaa atgcgatttc attaacattc ttaagctaata ata 445

<210> 62  
 <211> 114  
 <212> PRT  
 <213> Helicobacter pylori

<400> 62  
 Met Arg Phe Leu Asn Asn Lys His Arg Glu Lys Gly Leu Lys Ala Glu

09895913-062901

1	5	10	15
Glu Glu Ala Cys Gly Phe Leu Lys Ser Leu Gly Phe Glu Met Val Glu			
20	25	30	
Arg Asn Phe Phe Ser Gln Phe Gly Glu Ile Asp Ile Ile Ala Leu Lys			
35	40	45	
Lys Gly Val Leu His Phe Ile Glu Val Lys Ser Gly Glu Asn Phe Asp			
50	55	60	
Pro Ile Tyr Ala Ile Thr Pro Ser Lys Leu Lys Lys Met Ile Lys Thr			
65	70	75	80
Ile Arg Cys Tyr Leu Ser Gln Lys Asp Pro Asn Ser Asp Phe Cys Ile			
85	90	95	
Asp Ala Leu Ile Val Lys Asn Gly Lys Phe Glu Leu Leu Glu Asn Ile			
100	105	110	
Thr Phe			

<210> 63  
 <211> 831  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (86)...(763)

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caataaggct tagagaaaact ttttc atg gaa cac aga gta ttt act att gct	112
Met Glu His Arg Val Phe Thr Ile Ala	
1 5	
aat ttt ttt agc tcc aat cat gat ttt atc acc ggg ttt ttt gtc gtt	160
Asn Phe Phe Ser Ser Asn His Asp Phe Ile Thr Gly Phe Phe Val Val	
10 15 20 25	
ttg aca gcg gtt ttg atg ttt tta atc tcg ctt ggc gcg tcg cgc aaa	208
Leu Thr Ala Val Leu Met Phe Leu Ile Ser Leu Gly Ala Ser Arg Lys	
30 35 40	
atg cag atg gta cct atg ggt ttg cag aat gtg tat gag agc atc att	256
Met Gln Met Val Pro Met Gly Leu Gln Asn Val Tyr Glu Ser Ile Ile	
45 50 55	
agc gcg att ttg agc gtg gct aag gat att ata ggc gaa gaa tta gcc	304
Ser Ala Ile Leu Ser Val Ala Lys Asp Ile Ile Gly Glu Glu Leu Ala	
60 65 70	
cgc aaa tac ttc ccc cta gct ggc acg atc gct ttg tat gtc ttt ttt	352
Arg Lys Tyr Phe Pro Leu Ala Gly Thr Ile Ala Leu Tyr Val Phe Phe	
75 80 85	
tct aac atg ata ggc atc att cct ggc ttt gaa tcc cct acg gct agc	400
Ser Asn Met Ile Gly Ile Ile Pro Gly Phe Glu Ser Pro Thr Ala Ser	
90 95 100 105	
tgg agc ttt acg ctg gtt tta gcg ctg att gtg ttt ttt tat tac cat	448
Trp Ser Phe Thr Leu Val Leu Ala Leu Ile Val Phe Phe Tyr Tyr His	
110 115 120	

ttt gaa ggc att aga gtg cag ggc ttt ttt aag tat ttc gct cat ttt	496
Phe Glu Gly Ile Arg Val Gln Gly Phe Phe Lys Tyr Phe Ala His Phe	
125 130 135	
gca ggt cct gtg aaa tgg ctc gcc cct ttc atg ttc cct att gag atc	544
Ala Gly Pro Val Lys Trp Leu Ala Pro Phe Met Phe Pro Ile Glu Ile	
140 145 150	
atc tcg cat ttt tct agg atc gtg tct tta tcg ttt cgt ttg ttt ggg	592
Ile Ser His Phe Ser Arg Ile Val Ser Leu Ser Phe Arg Leu Phe Gly	
155 160 165	
aat atc aag ggc gat gac atg ttc ttg ctc atc atg ctt tta tta gtg	640
Asn Ile Lys Gly Asp Asp Met Phe Leu Leu Ile Met Leu Leu Leu Val	
170 175 180 185	
cct tgg gcg gtt cct gta gcg cct ttt atg gtg ttg ttt ttc atg ggg	688
Pro Trp Ala Val Pro Val Ala Pro Phe Met Val Leu Phe Phe Met Gly	
190 195 200	
att tta caa gct ttt gtt ttt atg atc ctc act tat gtg tat ttg gca	736
Ile Leu Gln Ala Phe Val Phe Met Ile Leu Thr Tyr Val Tyr Leu Ala	
205 210 215	
ggg gct gtt tta acc gat gaa ggg cat taagcaataa cattcttgtt	783
Gly Ala Val Leu Thr Asp Glu Gly His	
220 225	
tggtctttaat attgtttttt aaaactttgt tttatggtaa agcttttta	831
<210> 64	
<211> 226	
<212> PRT	
<213> Helicobacter pylori	
<400> 64	
Met Glu His Arg Val Phe Thr Ile Ala Asn Phe Phe Ser Ser Asn His	
1 5 10 15	
Asp Phe Ile Thr Gly Phe Phe Val Val Leu Thr Ala Val Leu Met Phe	
20 25 30	
Leu Ile Ser Leu Gly Ala Ser Arg Lys Met Gln Met Val Pro Met Gly	
35 40 45	
Leu Gln Asn Val Tyr Glu Ser Ile Ile Ser Ala Ile Leu Ser Val Ala	
50 55 60	
Lys Asp Ile Ile Gly Glu Glu Leu Ala Arg Lys Tyr Phe Pro Leu Ala	
65 70 75 80	
Gly Thr Ile Ala Leu Tyr Val Phe Phe Ser Asn Met Ile Gly Ile Ile	
85 90 95	
Pro Gly Phe Glu Ser Pro Thr Ala Ser Trp Ser Phe Thr Leu Val Leu	
100 105 110	
Ala Leu Ile Val Phe Phe Tyr Tyr His Phe Glu Gly Ile Arg Val Gln	
115 120 125	
Gly Phe Phe Lys Tyr Phe Ala His Phe Ala Gly Pro Val Lys Trp Leu	
130 135 140	
Ala Pro Phe Met Phe Pro Ile Glu Ile Ile Ser His Phe Ser Arg Ile	
145 150 155 160	
Val Ser Leu Ser Phe Arg Leu Phe Gly Asn Ile Lys Gly Asp Asp Met	
165 170 175	
Phe Leu Leu Ile Met Leu Leu Leu Val Pro Trp Ala Val Pro Val Ala	

**SECRET**

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<220>  
<221> CDS  
<222> (51) ... (734)
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-75-

Ser	Pro	Ile	Thr	Gln	Ser	Asn	Leu	Lys	Arg	Leu	Lys	Asp	Ser	Asn	His		
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att	att	tta	gac	acc	aaa	aac	gcc	ctt	tta	gca	tgc	gac	act	aaa	ggc	584	
Ile	Ile	Leu	Asp	Thr	Lys	Asn	Ala	Leu	Leu	Ala	Cys	Asp	Thr	Lys	Gly		
		165					170					175					
gat	ggg	gcg	atg	gct	gag	cct	tta	gaa	atc	ctt	ttt	aaa	gcc	gct	caa	632	
Asp	Gly	Ala	Met	Ala	Glu	Pro	Leu	Glu	Ile	Leu	Phe	Lys	Ala	Ala	Gln		
	180					185					190						
acg	ctc	cta	aaa	gac	gct	tat	ttt	gaa	aac	aga	gaa	gtc	ata	gtc	atg	680	
Thr	Leu	Leu	Lys	Asp	Ala	Tyr	Phe	Glu	Asn	Arg	Glu	Val	Ile	Val	Met		
195				200						205					210		
ggc	ggc	gcg	agt	ata	gaa	aag	att	gac	agc	gtt	cga	acg	att	agc	aat	728	
Gly	Gly	Ala	Ser	Ile	Glu	Lys	Ile	Asp	Ser	Val	Arg	Thr	Ile	Ser	Asn		
			215					220					225				
act	ttc	tagcgggatt	caagcgagcg	ctttagcttt	ggcggttatat	tttaagggag	784										
Thr	Phe																

cca 787

<210> 66  
 <211> 228  
 <212> PRT  
 <213> Helicobacter pylori

<400> 66

Met	Asn	Phe	Leu	Glu	Asp	Leu	Phe	Tyr	Pro	Leu	Arg	Leu	Leu	Glu	Asn		
1			5						10					15			
Lys	Arg	Val	Leu	Leu	Leu	Val	Ser	Gly	Ser	Ile	Ala	Ala	Tyr	Lys	Ser		
		20						25					30				
Leu	Glu	Leu	Val	Arg	Leu	Leu	Phe	Lys	Ser	Gly	Ala	Ser	Ile	Gln	Val		
	35					40					45						
Val	Met	Ser	Lys	Gly	Ala	Lys	Lys	Phe	Ile	Lys	Pro	Leu	Ser	Phe	Glu		
	50					55					60						
Ala	Leu	Ser	His	His	Lys	Val	Leu	His	Asp	Arg	Asn	Glu	Lys	Trp	Tyr		
65				70					75					80			
Tyr	Asn	His	Gln	Asn	Ala	Leu	His	His	Asn	His	Ile	Ala	Cys	Ala	Ala		
			85					90					95				
Asn	Ala	Asp	Leu	Leu	Ile	Phe	Ala	Pro	Leu	Ser	Thr	Asn	Ser	Leu	Ser		
		100					105					110					
Lys	Ile	Ala	His	Ala	Leu	Ala	Asp	Asn	Ile	Val	Ser	Ala	Thr	Phe	Leu		
	115					120						125					
Ala	Cys	Ala	Ser	Pro	Lys	Ile	Leu	Ala	Pro	Ser	Met	Asn	Thr	Asn	Met		
	130				135					140							
Leu	Asn	Ser	Pro	Ile	Thr	Gln	Ser	Asn	Leu	Lys	Arg	Leu	Lys	Asp	Ser		
145				150					155					160			
Asn	His	Ile	Ile	Leu	Asp	Thr	Lys	Asn	Ala	Leu	Leu	Ala	Cys	Asp	Thr		
			165					170					175				
Lys	Gly	Asp	Gly	Ala	Met	Ala	Glu	Pro	Leu	Glu	Ile	Leu	Phe	Lys	Ala		
	180					185						190					
Ala	Gln	Thr	Leu	Leu	Lys	Asp	Ala	Tyr	Phe	Glu	Asn	Arg	Glu	Val	Ile		
	195					200					205						
Val	Met	Gly	Gly	Ala	Ser	Ile	Glu	Lys	Ile	Asp	Ser	Val	Arg	Thr	Ile		
	210					215				220							



Ser Asn Thr Phe  
225

<210> 67  
<211> 1078  
<212> DNA  
<213> Helicobacter pylori

<220>  
<221> CDS  
<222> (71)...(1009)

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cgagcaaaaa atg aaa ccg caa gac att gaa atc gtt caa agc gtt tta 109  
Met Lys Pro Gln Asp Ile Glu Ile Val Gln Ser Val Leu  
1 5 10  
gag att aca gga ccg att aag cct act gaa gtg tat gat aaa gcc aaa 157  
Glu Ile Thr Gly Pro Ile Lys Pro Thr Glu Val Tyr Asp Lys Ala Lys  
15 20 25  
gag ctt ttt gaa aaa ggt gag att aca aac atg ttt gat tgt ggg ggc 205  
Glu Leu Phe Glu Lys Gly Glu Ile Thr Asn Met Phe Asp Cys Gly Gly  
30 35 40 45  
aaa acc ccg cac cag agc gtt agt tct tat att tat aca gcc tta aac 253  
Lys Thr Pro His Gln Ser Val Ser Ser Tyr Ile Tyr Thr Ala Leu Asn  
50 55 60  
aag ggc gaa gaa ctg cct ttt aaa aaa gtg caa gaa aac cca acc tta 301  
Lys Gly Glu Glu Leu Pro Phe Lys Lys Val Gln Glu Asn Pro Thr Leu  
65 70 75  
atc gct tta aaa gac gcg gct aaa gag cta ggt tta gac gct caa aaa 349  
Ile Ala Leu Lys Asp Ala Ala Lys Glu Leu Gly Leu Asp Ala Gln Lys  
80 85 90  
ata agc gct cca agc tct aaa atc gcg cat gaa agg gat ttg cac ccc 397  
Ile Ser Ala Pro Ser Ser Lys Ile Ala His Glu Arg Asp Leu His Pro  
95 100 105  
ttt tta acc tac atg gct att aat aac gaa aat ttg aaa tgc tac acg 445  
Phe Leu Thr Tyr Met Ala Ile Asn Asn Glu Asn Leu Lys Cys Tyr Thr  
110 115 120 125  
aaa acc att ttt cat gaa gag agt tca aaa tca ata aaa ggc atg gac 493  
Lys Thr Ile Phe His Glu Glu Ser Ser Lys Ser Ile Lys Gly Met Asp  
130 135 140  
agg tgg ctt tat ccg gac atg gtg ggg gtt agg ttt ttg cac gct gaa 541  
Arg Trp Leu Tyr Pro Asp Met Val Gly Val Arg Phe Leu His Ala Glu  
145 150 155  
tta tct aat gaa aat tta atc gct ttt tct aag aaa ttt gac act tta 589  
Leu Ser Asn Glu Asn Leu Ile Ala Phe Ser Lys Lys Phe Asp Thr Leu  
160 165 170  
ccc att aaa ctg gtg agc ttt gaa ttg aaa aaa gaa atc agc gtg cat 637

05395913-062901



Phe His Glu Glu Ser Ser Lys Ser Ile Lys Gly Met Asp Arg Trp Leu  
 130 135 140  
 Tyr Pro Asp Met Val Gly Val Arg Phe Leu His Ala Glu Leu Ser Asn  
 145 150 155 160  
 Glu Asn Leu Ile Ala Phe Ser Lys Lys Phe Asp Thr Leu Pro Ile Lys  
 165 170 175  
 Leu Val Ser Phe Glu Leu Lys Lys Glu Ile Ser Val His Asn Cys Arg  
 180 185 190  
 Glu Cys Tyr Phe Gln Ala Ile Ser Asn Ser Ser Trp Ala Asn Glu Gly  
 195 200 205  
 Tyr Leu Val Gly Arg His Ile Asp Thr His Asn Pro Gln Leu Met Asp  
 210 215 220  
 Leu Leu Lys Arg Leu His Ala Ser Phe Gly Ile Gly Val Ile Asp Leu  
 225 230 235 240  
 Arg Thr Asn Glu Asp Lys Ser Ala Ile Leu Leu Asn Ala Lys Tyr Lys  
 245 250 255  
 Glu Lys Ile Asp Tyr Thr Val Ala Ser Glu Leu Ser Ala Lys Asn Glu  
 260 265 270  
 Lys Phe Ser Gly Phe Leu Lys Ser Val Val Asp Tyr Asp Pro Asn His  
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 Leu Tyr Pro Asn Pro Ser Leu Ser Phe  
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 Met Lys  
 1  
 gct caa aaa agc ggg gtt tat aat gtg ggt tat tcc caa gcc aga agt 165  
 Ala Gln Lys Ser Gly Val Tyr Asn Val Gly Tyr Ser Gln Ala Arg Ser  
 5 10 15  
 tat aat gaa atc gtt agc att tta aaa gag cat tta ggg gat ttt aaa 213  
 Tyr Asn Glu Ile Val Ser Ile Leu Lys Glu His Leu Gly Asp Phe Lys  
 20 25 30  
 gtg agt tat atc aaa aac cct tat gct ttc ttc caa aag cac acc caa 261  
 Val Ser Tyr Ile Lys Asn Pro Tyr Ala Phe Phe Gln Lys His Thr Gln  
 35 40 45 50  
 gca cac att gag cct gct att ttg gat ttg gat tac acc cct tta tac 309  
 Ala His Ile Glu Pro Ala Ile Leu Asp Leu Asp Tyr Thr Pro Leu Tyr  
 55 60 65  
 gat ttg gaa agc ggc att aaa gat tat ttg ccc cat atc cat gcg att 357  
 Asp Leu Glu Ser Gly Ile Lys Asp Tyr Leu Pro His Ile His Ala Ile  
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405

444

<400> 70

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<400> 71

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aaa gcc ctt ttt ttg gac aga gac ggc att atc aat att gat aaa ggc 269  
Lys Ala Leu Phe Leu Asp Arg Asp Gly Ile Ile Asn Ile Asp Lys Gly  
25 30 35

tat gtg agt caa aaa gaa gat ttt gag ttt caa aaa ggg att ttt gaa 317  
Tyr Val Ser Gln Lys Glu Asp Phe Glu Phe Gln Lys Gly Ile Phe Glu  
40 45 50 55

ttg	cta	aag	cat	gcg	aaa	tct	tta	ggc	tac	aaa	ctg	ctt	tta	atc	acc	365
Leu	Leu	Lys	His	Ala	Lys	Ser	Leu	Gly	Tyr	Lys	Leu	Leu	Leu	Ile	Thr	
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aac caa tct ggg atc aac cga ggc tat tac acc ctt aaa gat ttt gaa 413

[illegible]

Asn	Gln	Ser	Gly	Ile	Asn	Arg	Gly	Tyr	Tyr	Thr	Leu	Lys	Asp	Phe	Glu		
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caa	ctc	acc	caa	tac	ctc	caa	gaa	agc	ttg	ttc	aaa	gaa	tta	ggg	ttt	461	
Gln	Leu	Thr	Gln	Tyr	Leu	Gln	Glu	Ser	Leu	Phe	Lys	Glu	Leu	Gly	Phe		
			90				95					100					
aat	ctg	gat	ggc	atc	tat	ttt	tgc	agg	cac	gcc	cca	gaa	gaa	aat	tgc	509	
Asn	Leu	Asp	Gly	Ile	Tyr	Phe	Cys	Arg	His	Ala	Pro	Glu	Glu	Asn	Cys		
			105			110					115						
gct	tgc	agg	aag	cca	aag	cct	tct	ttg	att	ttg	caa	gct	gct	aaa	gag	557	
Ala	Cys	Arg	Lys	Pro	Lys	Pro	Ser	Leu	Ile	Leu	Gln	Ala	Ala	Lys	Glu		
					125					130					135		
cat	caa	att	tgc	ttg	gag	caa	tct	ttt	atg	ata	ggc	gat	aaa	gag	agc	605	
His	Gln	Ile	Cys	Leu	Glu	Gln	Ser	Phe	Met	Ile	Gly	Asp	Lys	Glu	Ser		
				140					145					150			
gac	atg	tta	gcc	ggc	ttg	aac	gct	aaa	gtt	aaa	aat	aac	ctt	ttg	ctc	653	
Asp	Met	Leu	Ala	Gly	Leu	Asn	Ala	Lys	Val	Lys	Asn	Asn	Leu	Leu	Leu		
			155					160					165				
att	caa	aac	cct	tta	aaa	act	cct	cat	tct	tgg	ata	caa	tgt	aaa	gat	701	
Ile	Gln	Asn	Pro	Leu	Lys	Thr	Pro	His	Ser	Trp	Ile	Gln	Cys	Lys	Asp		
			170				175					180					
ttt	aaa	gag	atg	ata	gat	cta	atc	aaa	taaggacaag	aatgcgttat						748	
Phe	Lys	Glu	Met	Ile	Asp	Leu	Ile	Lys									
			185			190											
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Cys	Ile	Arg	Met	Asn	Thr	Asn	Lys	Ala	Leu	Phe	Leu	Asp	Arg	Asp	Gly		
			20					25					30				
Ile	Ile	Asn	Ile	Asp	Lys	Gly	Tyr	Val	Ser	Gln	Lys	Glu	Asp	Phe	Glu		
		35				40						45					
Phe	Gln	Lys	Gly	Ile	Phe	Glu	Leu	Leu	Lys	His	Ala	Lys	Ser	Leu	Gly		
	50				55					60							
Tyr	Lys	Leu	Leu	Leu	Ile	Thr	Asn	Gln	Ser	Gly	Ile	Asn	Arg	Gly	Tyr		
65					70					75				80			
Tyr	Thr	Leu	Lys	Asp	Phe	Glu	Gln	Leu	Thr	Gln	Tyr	Leu	Gln	Glu	Ser		
			85					90						95			
Leu	Phe	Lys	Glu	Leu	Gly	Phe	Asn	Leu	Asp	Gly	Ile	Tyr	Phe	Cys	Arg		
			100					105					110				
His	Ala	Pro	Glu	Glu	Asn	Cys	Ala	Cys	Arg	Lys	Pro	Lys	Pro	Ser	Leu		
		115					120					125					
Ile	Leu	Gln	Ala	Ala	Lys	Glu	His	Gln	Ile	Cys	Leu	Glu	Gln	Ser	Phe		
	130					135					140						
Met	Ile	Gly	Asp	Lys	Glu	Ser	Asp	Met	Leu	Ala	Gly	Leu	Asn	Ala	Lys		

145		150		155		160									
Val	Lys	Asn	Asn	Leu	Leu	Leu	Ile	Gln	Asn	Pro	Leu	Lys	Thr	Pro	His
			165					170						175	
Ser	Trp	Ile	Gln	Cys	Lys	Asp	Phe	Lys	Glu	Met	Ile	Asp	Leu	Ile	Lys
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 ctttagaaat gaataagaag taggcct atg cca gct agg caa tct ttt aca gat 114  
 Met Pro Ala Arg Gln Ser Phe Thr Asp  
 1 5

ttg aaa aac ctg gtt ttg tgc gat ata ggc aac acg cgt atc cat ttt 162  
 Leu Lys Asn Leu Val Leu Cys Asp Ile Gly Asn Thr Arg Ile His Phe  
 10 15 20 25

gca caa aac tat cag ctc ttt tca agc gct aaa gaa gat tta aag cgt 210  
 Ala Gln Asn Tyr Gln Leu Phe Ser Ser Ala Lys Glu Asp Leu Lys Arg  
 30 35 40

ttg ggt att caa aag gaa att ttt tac att agc gtg aat gaa gaa aat 258  
 Leu Gly Ile Gln Lys Glu Ile Phe Tyr Ile Ser Val Asn Glu Glu Asn  
 45 50 55

gaa aaa gcc ctt ttg aat tgt tac cct aac gct aaa aat att gca ggg 306  
 Glu Lys Ala Leu Leu Asn Cys Tyr Pro Asn Ala Lys Asn Ile Ala Gly  
 60 65 70

ttt ttt cat tta gaa acc gac tat gta ggg ctt ggg ata gac cgg caa 354  
 Phe Phe His Leu Glu Thr Asp Tyr Val Gly Leu Gly Ile Asp Arg Gln  
 75 80 85

atg gcg tgt ctg gcg gta aat aat ggc gtg gtg gtg gat gcc ggg agt 402  
 Met Ala Cys Leu Ala Val Asn Asn Gly Val Val Val Asp Ala Gly Ser  
 90 95 100 105

gcg att acg ata gat tta atc aaa gag ggc aag cat tta gga ggg tgt 450  
 Ala Ile Thr Ile Asp Leu Ile Lys Glu Gly Lys His Leu Gly Gly Cys  
 110 115 120

att tta ccc ggt tta gcc caa tat att cat gcg tat aaa aaa agc gct 498  
 Ile Leu Pro Gly Leu Ala Gln Tyr Ile His Ala Tyr Lys Lys Ser Ala  
 125 130 135

aaa att tta gag caa cct ttc aag gcc tta gat tct tta gaa gtt tta 546  
 Lys Ile Leu Glu Gln Pro Phe Lys Ala Leu Asp Ser Leu Glu Val Leu  
 140 145 150

cct aaa agc act aga gac gct gtg aat tac ggc atg gtt ttg agc gtc 594  
 Pro Lys Ser Thr Arg Asp Ala Val Asn Tyr Gly Met Val Leu Ser Val

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155

160

165

att gct tgt atc cag cat tta gcc aaa aat caa aaa atc tat ctt tgt 642  
 ile ala cys ile gln his leu ala lys asn gln lys ile tyr leu cys  
 170 175 180 185

ggg ggc gat gcg aag tat ttg agc gcg ttt tta ccc cat tct gtt tgc 690  
 gly gly asp ala lys tyr leu ser ala phe leu pro his ser val cys  
 190 195 200

aag gag cgt ttg gtt ttt gac ggg atg gaa atc gct ctt aaa aaa gca 738  
 lys glu arg leu val phe asp gly met glu ile ala leu lys lys ala  
 205 210 215

ggg ata cta gaa tgc aaa tgatgcacaa tttgagtttt ttgggcatgt 786  
 gly ile leu glu cys lys  
 220

ttttagccgc tttgagcatg tcttttagggc attgtgtggg catgt 831

&lt;210&gt; 74

&lt;211&gt; 223

&lt;212&gt; PRT

&lt;213&gt; Helicobacter pylori

&lt;400&gt; 74

Met Pro Ala Arg Gln Ser Phe Thr Asp Leu Lys Asn Leu Val Leu Cys  
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 Asp ile gly asn thr arg ile his phe ala gln asn tyr gln leu phe  
 20 25 30  
 Ser Ser ala lys glu asp leu lys arg leu gly ile gln lys glu ile  
 35 40 45  
 phe tyr ile ser val asn glu glu asn glu lys ala leu leu asn cys  
 50 55 60  
 tyr pro asn ala lys asn ile ala gly phe phe his leu glu thr asp  
 65 70 75 80  
 tyr val gly leu gly ile asp arg gln met ala cys leu ala val asn  
 85 90 95  
 asn gly val val val asp ala gly ser ala ile thr ile asp leu ile  
 100 105 110  
 lys glu gly lys his leu gly gly cys ile leu pro gly leu ala gln  
 115 120 125  
 tyr ile his ala tyr lys lys ser ala lys ile leu glu gln pro phe  
 130 135 140  
 lys ala leu asp ser leu glu val leu pro lys ser thr arg asp ala  
 145 150 155 160  
 val asn tyr gly met val leu ser val ile ala cys ile gln his leu  
 165 170 175  
 ala lys asn gln lys ile tyr leu cys gly gly asp ala lys tyr leu  
 180 185 190  
 ser ala phe leu pro his ser val cys lys glu arg leu val phe asp  
 195 200 205  
 gly met glu ile ala leu lys lys ala gly ile leu glu cys lys  
 210 215 220

&lt;210&gt; 75

&lt;211&gt; 1780

&lt;212&gt; DNA

&lt;213&gt; Helicobacter pylori

T06290"ET65850

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 <222> (195)...(1709)

<400> 75

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attatgtgat	aatcaccaca	agtaatcggc	ttagtgtcat	attacgaaga	tttaagatca	180
taaaaggaaa	aaag atg gtt	aat aaa gat	gtg aaa caa	acc act gct	ttt	230
	Met Val Asn	Lys Asp Val	Lys Gln Thr	Thr Ala Phe		
	1	5		10		
ggc gct ccc	gtt tgg gat	gac aac aat	gtg att acg	gcc ggc cct	aga	278
Gly Ala Pro	Val Trp Asp	Asp Asn Val	Ile Thr Ala	Gly Pro Arg		
	15	20		25		
ggt cct gtt	tta tta caa	agc act tgg	ttt ttg gaa	aag tta gcg	gcg	326
Gly Pro Val	Leu Leu Gln	Ser Thr Trp	Phe Leu Glu	Lys Leu Ala	Ala	
	30	35		40		
ttt gac aga	gaa aga atc	cct gaa agg	gtg gtg cat	gct aaa gga	agc	374
Phe Asp Arg	Glu Arg Ile	Pro Glu Arg	Val Val His	Ala Lys Gly	Ser	
	45	50		55	60	
gga gct tat	ggc act ttc	act gtg act	aaa gac atc	act aaa tac	act	422
Gly Ala Tyr	Gly Thr Phe	Thr Val Thr	Lys Asp Ile	Thr Lys Tyr	Thr	
	65		70		75	
aaa gcg aaa	att ttc tct	aaa gtg ggc	aaa aaa acc	gaa tgc ttc	ttc	470
Lys Ala Lys	Ile Phe Ser	Lys Val Gly	Lys Lys Thr	Glu Cys Phe	Phe	
	80	85		90		
aga ttt tct	act gtg gct	ggt gaa aga	ggc agt gcg	gat gcg gtg	aga	518
Arg Phe Ser	Thr Val Ala	Gly Glu Arg	Gly Ser Ala	Asp Ala Val	Arg	
	95	100		105		
gac cct aga	ggt ttt gcg	atg aag tat	tac act gaa	gaa ggt aac	tgg	566
Asp Pro Arg	Gly Phe Ala	Met Lys Tyr	Tyr Thr Glu	Glu Glu Gly	Asn Trp	
	110	115		120		
gat tta gtg	ggg aac aac	acg cct gtt	ttc ttt atc	cgt gat gcg	atc	614
Asp Leu Val	Gly Asn Asn	Thr Pro Val	Phe Phe Ile	Arg Asp Ala	Ile	
	125	130		135	140	
aaa ttc cct	gat ttc atc	cac act caa	aaa cga gat	cct caa acc	aat	662
Lys Phe Pro	Asp Phe Ile	His Thr Gln	Lys Arg Asp	Pro Gln Thr	Asn	
	145		150		155	
ttg cct aac	cat gac atg	gta tgg gat	ttt tgg agt	aat gtt cct	gaa	710
Leu Pro Asn	His Asp Met	Val Trp Asp	Phe Trp Ser	Asn Val Pro	Glu	
	160		165		170	
agc tta tac	caa gta aca	tgg gtt atg	agc gat agg	ggt att cct	aaa	758
Ser Leu Tyr	Gln Val Thr	Trp Val Met	Ser Asp Arg	Gly Ile Pro	Lys	
	175		180		185	
tct ttc cgc	cac atg gat	ggt ttt ggc	agc cac act	ttc agt ctt	atc	806
Ser Phe Arg	His Met Asp	Gly Phe Gly	Ser His Thr	Phe Ser Leu	Ile	
	190	195		200		

09095913 062904



aac gcg aaa ggc gaa cgc ttt tgg gtg aaa ttc cac ttt cac acc atg	854
Asn Ala Lys Gly Glu Arg Phe Trp Val Lys Phe His Phe His Thr Met	
205 210 215 220	
caa ggc gtt aag cat ttg act aac gaa gaa gcc gca gaa gtt agg aag	902
Gln Gly Val Lys His Leu Thr Asn Glu Glu Ala Ala Glu Val Arg Lys	
225 230 235	
tat gat ccg gat tcc aat caa agg gat tta ttc aat gcg atc gct aga	950
Tyr Asp Pro Asp Ser Asn Gln Arg Asp Leu Phe Asn Ala Ile Ala Arg	
240 245 250	
ggg gat ttc cca aaa tgg aaa tta agc att caa gtg atg cca gaa gaa	998
Gly Asp Phe Pro Lys Trp Lys Leu Ser Ile Gln Val Met Pro Glu Glu	
255 260 265	
gat gct aag aag tat cga ttc cat ccg ttt gat gta act aaa att tgg	1046
Asp Ala Lys Lys Tyr Arg Phe His Pro Phe Asp Val Thr Lys Ile Trp	
270 275 280	
tat ctc caa gat tat cca ttg atg gaa gtg ggc att gtg gag ttg aat	1094
Tyr Leu Gln Asp Tyr Pro Leu Met Glu Val Gly Ile Val Glu Leu Asn	
285 290 295 300	
aaa aat cct gaa aac tat ttc gca gaa gtg gaa caa gcg gca ttc agt	1142
Lys Asn Pro Glu Asn Tyr Phe Ala Glu Val Glu Gln Ala Ala Phe Ser	
305 310 315	
ccg gct aat gtc gtt cct gga att ggc tat agc cct gat agg atg tta	1190
Pro Ala Asn Val Val Pro Gly Ile Gly Tyr Ser Pro Asp Arg Met Leu	
320 325 330	
caa ggg cgc ttg ttc tct tat gga gac aca cac cgc tac cgc tta ggc	1238
Gln Gly Arg Leu Phe Ser Tyr Gly Asp Thr His Arg Tyr Arg Leu Gly	
335 340 345	
gtt aat tat cct caa ata ccg gtt aat aaa cca aga tgc cca ttc cac	1286
Val Asn Tyr Pro Gln Ile Pro Val Asn Lys Pro Arg Cys Pro Phe His	
350 355 360	
tct tct agc aga gat ggt tac atg caa aac gga tac tac ggc tct tta	1334
Ser Ser Ser Arg Asp Gly Tyr Met Gln Asn Gly Tyr Tyr Gly Ser Leu	
365 370 375 380	
caa aac tat acg cct agc tca ttg cct ggc tat aaa gaa gat aag agc	1382
Gln Asn Tyr Thr Pro Ser Ser Leu Pro Gly Tyr Lys Glu Asp Lys Ser	
385 390 395	
gcg aga gat cct aag ttc aac tta gct cat att gag aaa gag ttt gaa	1430
Ala Arg Asp Pro Lys Phe Asn Leu Ala His Ile Glu Lys Glu Phe Glu	
400 405 410	
gtg tgg aat tgg gat tac aga gct gat gat agc gat tac tac acc caa	1478
Val Trp Asn Trp Asp Tyr Arg Ala Asp Asp Ser Asp Tyr Tyr Thr Gln	
415 420 425	
cca ggt gat tac tac cgc tca ttg cca gct gat gaa aaa gaa agg ttg	1526
Pro Gly Asp Tyr Tyr Arg Ser Leu Pro Ala Asp Glu Lys Glu Arg Leu	

430

435

440

cat gac act att gga gag tct tta gct cat gtt acc cat aag gaa att 1574  
 His Asp Thr Ile Gly Glu Ser Leu Ala His Val Thr His Lys Glu Ile  
 445 450 455 460

gtg gat aaa caa ttg gag cat ttc aag aaa gct gac ccc aaa tac gct 1622  
 Val Asp Lys Gln Leu Glu His Phe Lys Lys Ala Asp Pro Lys Tyr Ala  
 465 470 475

gag gga gtt aaa aaa gct ctt gaa aaa cac caa aaa atg atg aaa gac 1670  
 Glu Gly Val Lys Lys Ala Leu Glu Lys His Gln Lys Met Met Lys Asp  
 480 485 490

atg cat gga aaa gac atg cac cac aca aaa aag aaa aag taaccctttt 1719  
 Met His Gly Lys Asp Met His His Thr Lys Lys Lys Lys  
 495 500 505

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 <212> PRT  
 <213> Helicobacter pylori

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 Leu Gln Ser Thr Trp Phe Leu Glu Lys Leu Ala Ala Phe Asp Arg Glu  
 35 40 45  
 Arg Ile Pro Glu Arg Val Val His Ala Lys Gly Ser Gly Ala Tyr Gly  
 50 55 60  
 Thr Phe Thr Val Thr Lys Asp Ile Thr Lys Tyr Thr Lys Ala Lys Ile  
 65 70 75 80  
 Phe Ser Lys Val Gly Lys Lys Thr Glu Cys Phe Phe Arg Phe Ser Thr  
 85 90 95  
 Val Ala Gly Glu Arg Gly Ser Ala Asp Ala Val Arg Asp Pro Arg Gly  
 100 105 110  
 Phe Ala Met Lys Tyr Tyr Thr Glu Glu Gly Asn Trp Asp Leu Val Gly  
 115 120 125  
 Asn Asn Thr Pro Val Phe Phe Ile Arg Asp Ala Ile Lys Phe Pro Asp  
 130 135 140  
 Phe Ile His Thr Gln Lys Arg Asp Pro Gln Thr Asn Leu Pro Asn His  
 145 150 155 160  
 Asp Met Val Trp Asp Phe Trp Ser Asn Val Pro Glu Ser Leu Tyr Gln  
 165 170 175  
 Val Thr Trp Val Met Ser Asp Arg Gly Ile Pro Lys Ser Phe Arg His  
 180 185 190  
 Met Asp Gly Phe Gly Ser His Thr Phe Ser Leu Ile Asn Ala Lys Gly  
 195 200 205  
 Glu Arg Phe Trp Val Lys Phe His Phe His Thr Met Gln Gly Val Lys  
 210 215 220  
 His Leu Thr Asn Glu Glu Ala Ala Glu Val Arg Lys Tyr Asp Pro Asp  
 225 230 235 240  
 Ser Asn Gln Arg Asp Leu Phe Asn Ala Ile Ala Arg Gly Asp Phe Pro  
 245 250 255

Lys Trp Lys Leu Ser Ile Gln Val Met Pro Glu Glu Asp Ala Lys Lys  
 260 265 270  
 Tyr Arg Phe His Pro Phe Asp Val Thr Lys Ile Trp Tyr Leu Gln Asp  
 275 280 285  
 Tyr Pro Leu Met Glu Val Gly Ile Val Glu Leu Asn Lys Asn Pro Glu  
 290 295 300  
 Asn Tyr Phe Ala Glu Val Glu Gln Ala Ala Phe Ser Pro Ala Asn Val  
 305 310 315 320  
 Val Pro Gly Ile Gly Tyr Ser Pro Asp Arg Met Leu Gln Gly Arg Leu  
 325 330 335  
 Phe Ser Tyr Gly Asp Thr His Arg Tyr Arg Leu Gly Val Asn Tyr Pro  
 340 345 350  
 Gln Ile Pro Val Asn Lys Pro Arg Cys Pro Phe His Ser Ser Ser Arg  
 355 360 365  
 Asp Gly Tyr Met Gln Asn Gly Tyr Tyr Gly Ser Leu Gln Asn Tyr Thr  
 370 375 380  
 Pro Ser Ser Leu Pro Gly Tyr Lys Glu Asp Lys Ser Ala Arg Asp Pro  
 385 390 395 400  
 Lys Phe Asn Leu Ala His Ile Glu Lys Glu Phe Glu Val Trp Asn Trp  
 405 410 415  
 Asp Tyr Arg Ala Asp Asp Ser Asp Tyr Tyr Thr Gln Pro Gly Asp Tyr  
 420 425 430  
 Tyr Arg Ser Leu Pro Ala Asp Glu Lys Glu Arg Leu His Asp Thr Ile  
 435 440 445  
 Gly Glu Ser Leu Ala His Val Thr His Lys Glu Ile Val Asp Lys Gln  
 450 455 460  
 Leu Glu His Phe Lys Lys Ala Asp Pro Lys Tyr Ala Glu Gly Val Lys  
 465 470 475 480  
 Lys Ala Leu Glu Lys His Gln Lys Met Met Lys Asp Met His Gly Lys  
 485 490 495  
 Asp Met His His Thr Lys Lys Lys Lys  
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<210> 77  
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 Asn Gly Phe Val Asn Ile Asn Asn Glu Lys Met Ser Lys Ser Leu Gly  
 5 10 15  
 aat agc ttt ttt gtt aaa gac gct ctc aaa aac tat gat ggc gaa att 152  
 Asn Ser Phe Phe Val Lys Asp Ala Leu Lys Asn Tyr Asp Gly Glu Ile  
 20 25 30  
 ttg cgc aat tac tta cta ggg gtg cat tat cgc tct gtt ttg aat ttc 200  
 Leu Arg Asn Tyr Leu Leu Gly Val His Tyr Arg Ser Val Leu Asn Phe  
 35 40 45 50

aat gaa gaa gac ttg tta gtg agt aaa aaa cgc ttg gat aaa atc tat 248  
 Asn Glu Glu Asp Leu Leu Val Ser Lys Lys Arg Leu Asp Lys Ile Tyr  
 55 60 65

cgt tta aaa cag cgc gtt tta ggg act ctt gga gga ata aat cca aac 296  
 Arg Leu Lys Gln Arg Val Leu Gly Thr Leu Gly Gly Ile Asn Pro Asn  
 70 75 80

ttt aaa aaa gaa att tta gag tgc atg caa gat gat tta aac gtt tct 344  
 Phe Lys Lys Glu Ile Leu Glu Cys Met Gln Asp Asp Leu Asn Val Ser  
 85 90 95

aaa gcg ttg agc gtt tta gaa agc atg ctt tct tcc act aat gaa aaa 392  
 Lys Ala Leu Ser Val Leu Glu Ser Met Leu Ser Ser Thr Asn Glu Lys  
 100 105 110

ttg gat caa aac cct aaa aac aag gct tta aag ggc gaa att tta gcg 440  
 Leu Asp Gln Asn Pro Lys Asn Lys Ala Leu Lys Gly Glu Ile Leu Ala  
 115 120 125 130

aat ttg aaa ttc ata gaa gaa ctg ctt ggc atc ggg ttt aaa gac cct 488  
 Asn Leu Lys Phe Ile Glu Glu Leu Leu Gly Ile Gly Phe Lys Asp Pro  
 135 140 145

agc gcc tat ttc caa tta ggc gtg agt gaa agc gaa aaa caa gaa att 536  
 Ser Ala Tyr Phe Gln Leu Gly Val Ser Glu Ser Glu Lys Gln Glu Ile  
 150 155 160

gaa aac aag ata gaa gaa aga aaa cgc gcc aaa gag cga aaa gat ttt 584  
 Glu Asn Lys Ile Glu Glu Arg Lys Arg Ala Lys Glu Arg Lys Asp Phe  
 165 170 175

tta aaa gcc gat agc atc aga gaa gag ctt ttg aaa caa aaa atc gct 632  
 Leu Lys Ala Asp Ser Ile Arg Glu Glu Leu Leu Lys Gln Lys Ile Ala  
 180 185 190

ttg atg gac acc cca caa ggc acg atc tgg gag aag ttt ttt 674  
 Leu Met Asp Thr Pro Gln Gly Thr Ile Trp Glu Lys Phe Phe  
 195 200 205

taaacacctc caattttacc tttttacaca ttctagcaac aacttttcagc att 727

<210> 78  
 <211> 208  
 <212> PRT  
 <213> Helicobacter pylori

<400> 78  
 Met His Asn Gly Phe Val Asn Ile Asn Asn Glu Lys Met Ser Lys Ser  
 1 5 10 15  
 Leu Gly Asn Ser Phe Phe Val Lys Asp Ala Leu Lys Asn Tyr Asp Gly  
 20 25 30  
 Glu Ile Leu Arg Asn Tyr Leu Leu Gly Val His Tyr Arg Ser Val Leu  
 35 40 45  
 Asn Phe Asn Glu Glu Asp Leu Leu Val Ser Lys Lys Arg Leu Asp Lys  
 50 55 60  
 Ile Tyr Arg Leu Lys Gln Arg Val Leu Gly Thr Leu Gly Gly Ile Asn  
 65 70 75 80  
 Pro Asn Phe Lys Lys Glu Ile Leu Glu Cys Met Gln Asp Asp Leu Asn

				85					90					95					
Val	Ser	Lys	Ala	Leu	Ser	Val	Leu	Glu	Ser	Met	Leu	Ser	Ser	Thr	Asn				
			100					105					110						
Glu	Lys	Leu	Asp	Gln	Asn	Pro	Lys	Asn	Lys	Ala	Leu	Lys	Gly	Glu	Ile				
		115					120					125							
Leu	Ala	Asn	Leu	Lys	Phe	Ile	Glu	Glu	Leu	Leu	Gly	Ile	Gly	Phe	Lys				
	130					135					140								
Asp	Pro	Ser	Ala	Tyr	Phe	Gln	Leu	Gly	Val	Ser	Glu	Ser	Glu	Lys	Gln				
145					150					155					160				
Glu	Ile	Glu	Asn	Lys	Ile	Glu	Glu	Arg	Lys	Arg	Ala	Lys	Glu	Arg	Lys				
			165					170						175					
Asp	Phe	Leu	Lys	Ala	Asp	Ser	Ile	Arg	Glu	Glu	Leu	Leu	Lys	Gln	Lys				
		180						185					190						
Ile	Ala	Leu	Met	Asp	Thr	Pro	Gln	Gly	Thr	Ile	Trp	Glu	Lys	Phe	Phe				
		195					200					205							

<210> 79  
 <211> 410  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (60)...(329)

<400> 79																			
ttttaaaagc atagaggatt ttaagaagca ttgtgaaaac ttataaataa gattttaaaa																		59	
atg ctg acg att gaa acc agt aaa aaa ttt gat aag gat ctt aaa att																		107	
Met Leu Thr Ile Glu Thr Ser Lys Lys Phe Asp Lys Asp Leu Lys Ile																			
1 5 10 15																			
ctt gtt aaa aac ggg ttt gat tta aag ctt ttg tat aaa gtg gtt gga																		155	
Leu Val Lys Asn Gly Phe Asp Leu Lys Leu Leu Tyr Lys Val Val Gly																			
20 25 30																			
aat tta gcc aca gag caa ccc cta gct ccc aaa tac aaa gac cac cca																		203	
Asn Leu Ala Thr Glu Gln Pro Leu Ala Pro Lys Tyr Lys Asp His Pro																			
35 40 45																			
ctc aaa ggc ggt tta aaa gat ttt agg gaa tgc cac tta aaa ccg gat																		251	
Leu Lys Gly Gly Leu Lys Asp Phe Arg Glu Cys His Leu Lys Pro Asp																			
50 55 60																			
tta ttg ctt gtc tat caa att aaa aaa caa gaa aac acc ctc ttt tta																		299	
Leu Leu Leu Val Tyr Gln Ile Lys Lys Gln Glu Asn Thr Leu Phe Leu																			
65 70 75 80																			
gta agg tta ggc agt cat agc gag ctg ttt tgaaccgccc acaccctta																		349	
Val Arg Leu Gly Ser His Ser Glu Leu Phe																			
85 90																			
taacgcttaa accaactacc cccctttttt agggataaat ttaggggttga aacaccgctt																		409	
a																		410	

<210> 80  
 <211> 90  
 <212> PRT  
 <213> Helicobacter pylori

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<400> 80  
 Met Leu Thr Ile Glu Thr Ser Lys Lys Phe Asp Lys Asp Leu Lys Ile  
 1 5 10 15  
 Leu Val Lys Asn Gly Phe Asp Leu Lys Leu Leu Tyr Lys Val Val Gly  
 20 25 30  
 Asn Leu Ala Thr Glu Gln Pro Leu Ala Pro Lys Tyr Lys Asp His Pro  
 35 40 45  
 Leu Lys Gly Gly Leu Lys Asp Phe Arg Glu Cys His Leu Lys Pro Asp  
 50 55 60  
 Leu Leu Leu Val Tyr Gln Ile Lys Lys Gln Glu Asn Thr Leu Phe Leu  
 65 70 75 80  
 Val Arg Leu Gly Ser His Ser Glu Leu Phe  
 85 90

<210> 81  
 <211> 425  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (78)...(341)

<400> 81  
 agatgtaggt aacaaagaga cagatttgat tgttgaggat ttttctagtt acagcaatga 60  
 aagaaaaagg gcttttag gtg ttg aag ctc aat ctt aaa aaa tct ttt caa 110  
 Val Leu Lys Leu Asn Leu Lys Lys Ser Phe Gln  
 1 5 10  
 aaa gat ttt gat aaa ttg ctt ttg aat ggg ttt gat gat agc gtt ttg 158  
 Lys Asp Phe Asp Lys Leu Leu Leu Asn Gly Phe Asp Asp Ser Val Leu  
 15 20 25  
 aat gaa gtc att cta acc tta aga aaa aaa gaa ccg cta gat cca caa 206  
 Asn Glu Val Ile Leu Thr Leu Arg Lys Lys Glu Pro Leu Asp Pro Gln  
 30 35 40  
 ttt caa gat cat gcc tta aag gga aag tgg aaa cct ttt agg gaa tgc 254  
 Phe Gln Asp His Ala Leu Lys Gly Lys Trp Lys Pro Phe Arg Glu Cys  
 45 50 55  
 cac att aag cct gat gtt ttg ctt gtg tat tta gtg aaa gat gat gaa 302  
 His Ile Lys Pro Asp Val Leu Leu Val Tyr Leu Val Lys Asp Asp Glu  
 60 65 70 75  
 ctg att ttg tta agg tta ggc agt cat agc gag ctg ttt taatccaccc 351  
 Leu Ile Leu Leu Arg Leu Gly Ser His Ser Glu Leu Phe  
 80 85  
 acacccctta taacgcttaa accaaatcgc ttgcgctata atgaactgat attatatattt 411  
 aaaaggaata aaca 425

<210> 82  
 <211> 88  
 <212> PRT  
 <213> Helicobacter pylori

<400> 82  
 Val Leu Lys Leu Asn Leu Lys Lys Ser Phe Gln Lys Asp Phe Asp Lys

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006591.062901E1656860

1	5	10	15
Leu Leu Leu Asn Gly Phe Asp Asp Ser Val Leu Asn Glu Val Ile Leu			
20	25	30	
Thr Leu Arg Lys Lys Glu Pro Leu Asp Pro Gln Phe Gln Asp His Ala			
35	40	45	
Leu Lys Gly Lys Trp Lys Pro Phe Arg Glu Cys His Ile Lys Pro Asp			
50	55	60	
Val Leu Leu Val Tyr Leu Val Lys Asp Asp Glu Leu Ile Leu Leu Arg			
65	70	75	80
Leu Gly Ser His Ser Glu Leu Phe			
85			

<210> 83  
 <211> 844  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (111)...(779)

<400> 83	
gtcgttatttc gcgcttaatg agaacagagg tttttaaaac tatggtttcg ttttaggttta	60
attaaatttc gctacaatta aataaaaacg ataatttttag agagattggc atg caa	116
	Met Gln
	1
ggt tta tgg att tat cca gag gat aca gaa gtt tta ggg gtt gct tgt	164
Gly Leu Trp Ile Tyr Pro Glu Asp Thr Glu Val Leu Gly Val Ala Cys	
5 10 15	
aag agc ctt tta aaa gca cta acg cca cgc tat caa aaa gtc gcc ttg	212
Lys Ser Leu Leu Lys Ala Leu Thr Pro Arg Tyr Gln Lys Val Ala Leu	
20 25 30	
ttt tcg ccc att agt gga ggg tgt gag agc ttg gag gag tgc gag agc	260
Phe Ser Pro Ile Ser Gly Gly Cys Glu Ser Leu Glu Glu Cys Glu Ser	
35 40 45 50	
ttg aac cct tta gaa ttt cat agt gcg ata agc aaa caa aag gct tta	308
Leu Asn Pro Leu Glu Phe His Ser Ala Ile Ser Lys Gln Lys Ala Leu	
55 60 65	
gag ctt gcg agc acc gct caa gaa gag tta cta ttt gaa acg att ctc	356
Glu Leu Ala Ser Thr Ala Gln Glu Glu Leu Leu Phe Glu Thr Ile Leu	
70 75 80	
aaa cgc tat gat gaa tta caa tcc acg cat gat ttt gtc att aat ttg	404
Lys Arg Tyr Asp Glu Leu Gln Ser Thr His Asp Phe Val Ile Asn Leu	
85 90 95	
ggg tgt gcg ccg aag ttt ttc tta aac gct cct tta gat tta aac acc	452
Gly Cys Ala Pro Lys Phe Phe Leu Asn Ala Pro Leu Asp Leu Asn Thr	
100 105 110	
att tta gcc aag cat tta aac gct tct gtt gtg gct gtc gcg caa acg	500
Ile Leu Ala Lys His Leu Asn Ala Ser Val Val Ala Val Ala Gln Thr	
115 120 125 130	

agt ttg gaa tat ttg aaa gcc atg cac tct cat att ctc aaa aaa gaa 548  
 Ser Leu Glu Tyr Leu Lys Ala Met His Ser His Ile Leu Lys Lys Glu  
 135 140 145

gcc cct ttc gct gta ggg tta ttt gcg ggc gaa acg ctt gaa aaa cca 596  
 Ala Pro Phe Ala Val Gly Leu Phe Ala Gly Glu Thr Leu Glu Lys Pro  
 150 155 160

cat ttt tta agc atg tct ctt tgc aag caa caa tgc gaa tta gaa gcg 644  
 His Phe Leu Ser Met Ser Leu Cys Lys Gln Gln Cys Glu Leu Glu Ala  
 165 170 175

gat ctg att gaa agc gtg ttg caa ata aaa agc gag att att acc cct 692  
 Asp Leu Ile Glu Ser Val Leu Gln Ile Lys Ser Glu Ile Ile Thr Pro  
 180 185 190

tta gcc ttt caa agg ggt ttg gaa aaa aag gct aaa aaa cag att aaa 740  
 Leu Ala Phe Gln Arg Gly Leu Glu Lys Lys Ala Lys Lys Gln Ile Lys  
 195 200 205 210

aaa gtg gtt tta cca gag agc gaa aag atg aaa gga ttt tgaaagctgc 789  
 Lys Val Val Leu Pro Glu Ser Glu Lys Met Lys Gly Phe  
 215 220

acatcgtttg aatttaatgg gcgcggtagg attgatctta ttaggcgata aagaa 844

<210> 84  
 <211> 223  
 <212> PRT  
 <213> Helicobacter pylori

<400> 84  
 Met Gln Gly Leu Trp Ile Tyr Pro Glu Asp Thr Glu Val Leu Gly Val  
 1 5 10 15  
 Ala Cys Lys Ser Leu Leu Lys Ala Leu Thr Pro Arg Tyr Gln Lys Val  
 20 25 30  
 Ala Leu Phe Ser Pro Ile Ser Gly Gly Cys Glu Ser Leu Glu Glu Cys  
 35 40 45  
 Glu Ser Leu Asn Pro Leu Glu Phe His Ser Ala Ile Ser Lys Gln Lys  
 50 55 60  
 Ala Leu Glu Leu Ala Ser Thr Ala Gln Glu Glu Leu Leu Phe Glu Thr  
 65 70 75 80  
 Ile Leu Lys Arg Tyr Asp Glu Leu Gln Ser Thr His Asp Phe Val Ile  
 85 90 95  
 Asn Leu Gly Cys Ala Pro Lys Phe Phe Leu Asn Ala Pro Leu Asp Leu  
 100 105 110  
 Asn Thr Ile Leu Ala Lys His Leu Asn Ala Ser Val Val Ala Val Ala  
 115 120 125  
 Gln Thr Ser Leu Glu Tyr Leu Lys Ala Met His Ser His Ile Leu Lys  
 130 135 140  
 Lys Glu Ala Pro Phe Ala Val Gly Leu Phe Ala Gly Glu Thr Leu Glu  
 145 150 155 160  
 Lys Pro His Phe Leu Ser Met Ser Leu Cys Lys Gln Gln Cys Glu Leu  
 165 170 175  
 Glu Ala Asp Leu Ile Glu Ser Val Leu Gln Ile Lys Ser Glu Ile Ile  
 180 185 190  
 Thr Pro Leu Ala Phe Gln Arg Gly Leu Glu Lys Lys Ala Lys Lys Gln  
 195 200 205  
 Ile Lys Lys Val Val Leu Pro Glu Ser Glu Lys Met Lys Gly Phe



210

215

220

&lt;210&gt; 85

&lt;211&gt; 821

&lt;212&gt; DNA

&lt;213&gt; Helicobacter pylori

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (79)...(753)

&lt;400&gt; 85

tatgcctgga	ggtttggtgt	ggatgcgtca	agataatttg	cgntacaac	cgcaatttaa	60
agccagaaat	tgggcaaa	atg tgg aat ttt aac acc gaa tac agc agt cag				111
	Met Trp Asn Phe Asn Thr Glu Tyr Ser Ser Gln					
	1		5		10	
tat ttt gat ttt aga gcc gcc ggt ttt gtc caa ttg att tct aat tac						159
Tyr Phe Asp Phe Arg Ala Ala Gly Phe Val Gln Leu Ile Ser Asn Tyr						
	15		20		25	
atc aat caa ttt tct tca acg ctt ttt gta acc aac ttg ccc gca caa						207
Ile Asn Gln Phe Ser Ser Thr Leu Phe Val Thr Asn Leu Pro Ala Gln						
	30		35		40	
gat att att tat gtg cct ggt tat gaa gtt tca ggg acg gct aaa tac						255
Asp Ile Ile Tyr Val Pro Gly Tyr Glu Val Ser Gly Thr Ala Lys Tyr						
	45		50		55	
aag ggc ttt tct tta ggc ttg agc gtg gcg cga tca tgg cct tct tta						303
Lys Gly Phe Ser Leu Gly Leu Ser Val Ala Arg Ser Trp Pro Ser Leu						
	60		65		70	75
aag ggg cgt ttg atc gct gat gtg tat gaa ttg gcg gcc acg aca ggc						351
Lys Gly Arg Leu Ile Ala Asp Val Tyr Glu Leu Ala Ala Thr Thr Gly						
	80		85		90	
aat gtg ttt att ttg acg gca agt tat aaa atc cca cgc act ggt ctt						399
Asn Val Phe Ile Leu Thr Ala Ser Tyr Lys Ile Pro Arg Thr Gly Leu						
	95		100		105	
agc atc act tgg ctt tca cgc ttc gtt acg gat ttg agt tat tgc tct						447
Ser Ile Thr Trp Leu Ser Arg Phe Val Thr Asp Leu Ser Tyr Cys Ser						
	110		115		120	
tat agc cct tat cgt aac ggc cct acg gat att gac aga cgg cct agt						495
Tyr Ser Pro Tyr Arg Asn Gly Pro Thr Asp Ile Asp Arg Arg Pro Ser						
	125		130		135	
aat tgc cct aaa acg ccc ggg att ttt cat gtt cat aaa ccc ggt tat						543
Asn Cys Pro Lys Thr Pro Gly Ile Phe His Val His Lys Pro Gly Tyr						
	140		145		150	155
ggg gtg agc agt ttt ttt gta acc tac aaa ccc acc tat aag aag ctt						591
Gly Val Ser Ser Phe Phe Val Thr Tyr Lys Pro Thr Tyr Lys Lys Leu						
	160		165		170	
aaa ggg ttg agc ttg aat gcg gtg ttt aac aat gtt ttt aac caa caa						639
Lys Gly Leu Ser Leu Asn Ala Val Phe Asn Asn Val Phe Asn Gln Gln						

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175	180	185	
tat att gat caa gca agc ccg gtg atg agc cct gat gaa ccc aat caa			687
Tyr Ile Asp Gln Ala Ser Pro Val Met Ser Pro Asp Glu Pro Asn Gln			
190	195	200	
gac aaa tac gca aga ggc atg gca gag cct ggc ttt aac gct aga ttt			735
Asp Lys Tyr Ala Arg Gly Met Ala Glu Pro Gly Phe Asn Ala Arg Phe			
205	210	215	
gaa att tcc tat aag ttt taataatgga tctaaaaata aggatttcat			783
Glu Ile Ser Tyr Lys Phe			
220	225		
gggtagcgga tctaatacaaa aataaaacat tcttttaga			821

<210> 86  
 <211> 225  
 <212> PRT  
 <213> Helicobacter pylori

<400> 86	
Met Trp Asn Phe Asn Thr Glu Tyr Ser Ser Gln Tyr Phe Asp Phe Arg	
1 5 10 15	
Ala Ala Gly Phe Val Gln Leu Ile Ser Asn Tyr Ile Asn Gln Phe Ser	
20 25 30	
Ser Thr Leu Phe Val Thr Asn Leu Pro Ala Gln Asp Ile Ile Tyr Val	
35 40 45	
Pro Gly Tyr Glu Val Ser Gly Thr Ala Lys Tyr Lys Gly Phe Ser Leu	
50 55 60	
Gly Leu Ser Val Ala Arg Ser Trp Pro Ser Leu Lys Gly Arg Leu Ile	
65 70 75 80	
Ala Asp Val Tyr Glu Leu Ala Ala Thr Thr Gly Asn Val Phe Ile Leu	
85 90 95	
Thr Ala Ser Tyr Lys Ile Pro Arg Thr Gly Leu Ser Ile Thr Trp Leu	
100 105 110	
Ser Arg Phe Val Thr Asp Leu Ser Tyr Cys Ser Tyr Ser Pro Tyr Arg	
115 120 125	
Asn Gly Pro Thr Asp Ile Asp Arg Arg Pro Ser Asn Cys Pro Lys Thr	
130 135 140	
Pro Gly Ile Phe His Val His Lys Pro Gly Tyr Gly Val Ser Ser Phe	
145 150 155 160	
Phe Val Thr Tyr Lys Pro Thr Tyr Lys Lys Leu Lys Gly Leu Ser Leu	
165 170 175	
Asn Ala Val Phe Asn Asn Val Phe Asn Gln Gln Tyr Ile Asp Gln Ala	
180 185 190	
Ser Pro Val Met Ser Pro Asp Glu Pro Asn Gln Asp Lys Tyr Ala Arg	
195 200 205	
Gly Met Ala Glu Pro Gly Phe Asn Ala Arg Phe Glu Ile Ser Tyr Lys	
210 215 220	
Phe	
225	

<210> 87  
 <211> 1350  
 <212> DNA  
 <213> Helicobacter pylori  
 <220>

<221> CDS  
 <222> (60)...(1202)

<400> 87

aattttgaaa acattgactc agttttcgctc tcaagggcgt ttaattcaag gatcaaagc	59
atg aat tta aat ttt atg ccc cta ttg cat gct tat aac cat gcg agc	107
Met Asn Leu Asn Phe Met Pro Leu Leu His Ala Tyr Asn His Ala Ser	
1 5 10 15	
att gat ttt cat ttc aat tct agt gct agg gat ttt tgc gtg cat gaa	155
Ile Asp Phe His Phe Asn Ser Ser Ala Arg Asp Phe Cys Val His Glu	
20 25 30	
gtg cct ttg tat gaa ttt agt aac acg ggc gaa cat gcc gtt att caa	203
Val Pro Leu Tyr Glu Phe Ser Asn Thr Gly Glu His Ala Val Ile Gln	
35 40 45	
gtg agg aaa agc ggt tta agc act tta gaa atg ctt cag att ttt tct	251
Val Arg Lys Ser Gly Leu Ser Thr Leu Glu Met Leu Gln Ile Phe Ser	
50 55 60	
caa att tta ggg gta aga atc gct gaa ttg ggt tat gcg ggc ttg aaa	299
Gln Ile Leu Gly Val Arg Ile Ala Glu Leu Gly Tyr Ala Gly Leu Lys	
65 70 75 80	
gat aaa aac gcg ctg acg act caa ttc atc tca ctc cct aaa aaa tac	347
Asp Lys Asn Ala Leu Thr Thr Gln Phe Ile Ser Leu Pro Lys Lys Tyr	
85 90 95	
gcc cct tta tta gaa aaa aat acg agc aac ttt caa gaa aaa aac ctt	395
Ala Pro Leu Leu Glu Lys Asn Thr Ser Asn Phe Gln Glu Lys Asn Leu	
100 105 110	
aaa atc ctg tct ttg aat tac cac cac aat aaa atc aaa ttg ggg cat	443
Lys Ile Leu Ser Leu Asn Tyr His His Asn Lys Ile Lys Leu Gly His	
115 120 125	
ttg aaa ggg aat cgc ttt ttt atg cgt ttt aaa aaa atg acc cct cta	491
Leu Lys Gly Asn Arg Phe Phe Met Arg Phe Lys Lys Met Thr Pro Leu	
130 135 140	
aac gct caa aaa aca aag cag gtt tta gaa caa atc gcg cag ttt gga	539
Asn Ala Gln Lys Thr Lys Gln Val Leu Glu Gln Ile Ala Gln Phe Gly	
145 150 155 160	
atg cct aat tat ttt ggc tcg caa cgc ttt ggg aag ttc aat gac aac	587
Met Pro Asn Tyr Phe Gly Ser Gln Arg Phe Gly Lys Phe Asn Asp Asn	
165 170 175	
cac caa gag ggt tta aaa atc tta caa aat caa acg aaa ttc gcc cat	635
His Gln Glu Gly Leu Lys Ile Leu Gln Asn Gln Thr Lys Phe Ala His	
180 185 190	
caa aaa tta aac gct ttt tta att tca agc tat caa agt tat ttg ttt	683
Gln Lys Leu Asn Ala Phe Leu Ile Ser Ser Tyr Gln Ser Tyr Leu Phe	
195 200 205	
aac gcg ctt tta agc aaa cga tta gaa atc agt aaa atc att agc gct	731
Asn Ala Leu Leu Ser Lys Arg Leu Glu Ile Ser Lys Ile Ile Ser Ala	

210	215	220	
ttt agt gtc aaa gaa aat tta gaa ttt ttt aaa caa aaa aat tta agc			779
Phe Ser Val Lys Glu Asn Leu Glu Phe Phe Lys Gln Lys Asn Leu Ser			
225	230	235	240
ggt gat tca gac act cta aaa acc ctt aaa aac caa gcc cac ccc ttt			827
Val Asp Ser Asp Thr Leu Lys Thr Leu Lys Asn Gln Ala His Pro Phe			
	245	250	255
aaa atc tta gaa ggc gat gtg atg tgc cat tac cct tat ggg aag ttt			875
Lys Ile Leu Glu Gly Asp Val Met Cys His Tyr Pro Tyr Gly Lys Phe			
	260	265	270
ttt gac gct tta gaa tta gaa aaa gag ggc gaa agg ttt ttg aaa aaa			923
Phe Asp Ala Leu Glu Leu Glu Lys Glu Gly Glu Arg Phe Leu Lys Lys			
	275	280	285
gaa gtt gcg cct acg ggg tta cta gac ggc aaa aaa gct ctt tat gca			971
Glu Val Ala Pro Thr Gly Leu Leu Asp Gly Lys Lys Ala Leu Tyr Ala			
	290	295	300
aaa aat ttg agt tta gaa att gaa aaa gaa ttc cag cat aac ctt tta			1019
Lys Asn Leu Ser Leu Glu Ile Glu Lys Glu Phe Gln His Asn Leu Leu			
	305	310	315
agt agc cat gct aaa acg cta ggc tct agg cgg ttt ttt tgg gtg ttt			1067
Ser Ser His Ala Lys Thr Leu Gly Ser Arg Arg Phe Phe Trp Val Phe			
	325	330	335
gta gaa aat gta act tct caa tac gtg aaa gaa aaa gcg caa ttt gaa			1115
Val Glu Asn Val Thr Ser Gln Tyr Val Lys Glu Lys Ala Gln Phe Glu			
	340	345	350
ttg gga ttt tac ttg cct aaa ggg agt tat gcg agc gcg ttg ctc aaa			1163
Leu Gly Phe Tyr Leu Pro Lys Gly Ser Tyr Ala Ser Ala Leu Leu Lys			
	355	360	365
gaa atc aag cat gag aaa gga gaa aat aat gac gaa ttt tgaaaagatt			1212
Glu Ile Lys His Glu Lys Gly Glu Asn Asn Asp Glu Phe			
	370	375	380
atcgcgcaaa acaggatcaa aacgaacgcg gtttttagcga cttattgcgt gattttttgct			1272
tttatcgggt tgttggtgga tgtcattaga attaattgcta atgatttagg aatagctctt			1332
tttaaactca tgactttt			1350

<210> 88  
 <211> 381  
 <212> PRT  
 <213> Helicobacter pylori

<400> 88  
 Met Asn Leu Asn Phe Met Pro Leu Leu His Ala Tyr Asn His Ala Ser  
 1 5 10 15  
 Ile Asp Phe His Phe Asn Ser Ser Ala Arg Asp Phe Cys Val His Glu  
 20 25 30  
 Val Pro Leu Tyr Glu Phe Ser Asn Thr Gly Glu His Ala Val Ile Gln  
 35 40 45  
 Val Arg Lys Ser Gly Leu Ser Thr Leu Glu Met Leu Gln Ile Phe Ser

	50					55					60					
Gln 65	Ile	Leu	Gly	Val	Arg 70	Ile	Ala	Glu	Leu	Gly 75	Tyr	Ala	Gly	Leu	Lys 80	
Asp	Lys	Asn	Ala	Leu 85	Thr	Thr	Gln	Phe	Ile 90	Ser	Leu	Pro	Lys	Lys 95	Tyr	
Ala	Pro	Leu	Leu 100	Glu	Lys	Asn	Thr	Ser 105	Asn	Phe	Gln	Glu	Lys 110	Asn	Leu	
Lys	Ile	Leu 115	Ser	Leu	Asn	Tyr	His 120	His	Asn	Lys	Ile	Lys 125	Leu	Gly	His	
Leu	Lys 130	Gly	Asn	Arg	Phe	Phe 135	Met	Arg	Phe	Lys	Lys 140	Met	Thr	Pro	Leu	
Asn 145	Ala	Gln	Lys	Thr	Lys 150	Gln	Val	Leu	Glu	Gln 155	Ile	Ala	Gln	Phe	Gly 160	
Met	Pro	Asn	Tyr	Phe 165	Gly	Ser	Gln	Arg	Phe 170	Gly	Lys	Phe	Asn	Asp 175	Asn	
His	Gln	Glu	Gly 180	Leu	Lys	Ile	Leu	Gln 185	Asn	Gln	Thr	Lys	Phe 190	Ala	His	
Gln	Lys	Leu 195	Asn	Ala	Phe	Leu	Ile 200	Ser	Ser	Tyr	Gln	Ser 205	Tyr	Leu	Phe	
Asn 210	Ala	Leu 215	Leu	Ser	Lys	Arg	Leu 220	Glu	Ile	Ser	Lys 225	Ile	Ile	Ser	Ala	
Phe 225	Ser	Val	Lys	Glu	Asn 230	Leu	Glu	Phe	Phe 235	Lys	Gln	Lys	Asn	Leu	Ser 240	
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Phe	Asp	Ala 275	Leu	Glu	Leu	Glu	Lys 280	Glu	Gly	Glu	Arg	Phe 285	Leu	Lys	Lys	
Glu	Val 290	Ala	Pro	Thr	Gly	Leu 295	Leu	Asp	Gly	Lys	Lys 300	Ala	Leu	Tyr	Ala	
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Ser	Ser	His	Ala	Lys 325	Thr	Leu	Gly	Ser	Arg 330	Arg	Phe	Phe	Trp	Val 335	Phe	
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Leu	Gly	Phe 355	Tyr	Leu	Pro	Lys	Gly 360	Ser	Tyr	Ala	Ser	Ala 365	Leu	Leu	Lys	
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- 97 -



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35 40 45  
Leu Thr Gly Cys Asp Ser Leu Tyr Ala Val His Pro Lys Phe Lys Thr  
50 55 60  
Ser Trp Asp Tyr Tyr Asn Glu Pro Lys Pro Leu Ile Glu Arg Leu Glu  
65 70 75 80  
Asp Leu Ala Pro Asn Tyr Lys Asp Phe Asp Phe Ile Leu Thr Gly Gly  
85 90 95  
Glu Pro Ser Leu Tyr Phe Asn Asn Pro Ile Leu Ile Ser Val Leu Glu  
100 105 110  
His Phe Tyr Arg Gln Lys Ile Pro Leu Cys Val Glu Ser Asn Gly Ser  
115 120 125  
Ile Phe Phe Glu Phe Ser Pro Ile Leu Lys Glu Leu His Phe Thr Leu  
130 135 140  
Ser Val Lys Leu Ser Phe Ser Leu Glu Glu Glu Ser Lys Arg Ile His  
145 150 155 160  
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165 170 175  
Lys Phe Val Leu Glu Ser Gln Asn Ala Ala Gln Ser Ile Ile Glu Ile  
180 185 190  
Gln Ser Leu Leu Lys Gln Leu Ser Leu Lys Asn Asn Glu Ile Phe Leu  
195 200 205  
Met Pro Leu Gly Thr Asn Asn Asn Glu Leu Asp Lys Asn Leu Lys Thr  
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g a t t t t a t t c g g t g g g a t t g t c a g c a t c a a g c c t c a t t g t t c c t a t t a g c g t t a t t t t a 119  
a t g g t g g t t t t a c t a a a a g a g t c g c a c t c t c g t t a t t t g t g g g c a t t 167  
Met Val Val Phe Thr Lys Arg Val Ala Leu Ser Leu Phe Val Gly Ile  
1 5 10 15

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gaa	tat	att	tat	cat	aaa	atc	act	tcc	gtt	ttt	tac	act	tac	gag	cca	263
Glu	Tyr	Ile	Tyr	His	Lys	Ile	Thr	Ser	Val	Phe	Tyr	Thr	Tyr	Glu	Pro	
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gaa	aag	ggg	ctt	aat	ttc	aat	ctt	tcc	aac	ctc	tat	gtt	ttt	ggg	ttt	311
Glu	Lys	Gly	Leu	Asn	Phe	Asn	Leu	Ser	Asn	Leu	Tyr	Val	Phe	Gly	Phe	
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Val	Gln	Asn	Phe	Val	Lys	Lys	Ala	Lys	Lys	Tyr	Ser	Lys	Asn	Ala	Lys	
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Thr	Ser	Ala	Pro	Val	Cys	Leu	Leu	Val	Pro	Ile	Ser	Ser	Trp	Gly	Ala	
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Ser	Phe	Ser	Val	Leu	Val	Gln	Ser	Leu	Ser	Ser	Asn	Tyr	Tyr	Ala	Ile	
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Phe	Ala	Leu	Ile	Ala	Val	Phe	Leu	Thr	Ile	Leu	Trp	Gln	Ile	Asn	Leu	
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cct	agc	atg	aga	aag	tat	caa	aac	ata	ggc	gtg	aag	gat	ttt	tat	agc	791
Pro	Ser	Met	Arg	Lys	Tyr	Gln	Asn	Ile	Gly	Val	Lys	Asp	Phe	Tyr	Ser	
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Glu	Gln	Glu	Glu	Ser	Ser	Ser	Lys	Leu	Ala	Pro	Leu	Ser	Leu	Leu	Pro	
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Lys	Gly	Phe	Leu	Asn	Asn	Gly	Gly	Gly	Val	Tyr	Met	Pro	Leu	Ile	Phe					
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Gly	Val	Phe	Tyr	Leu	Leu	Lys	Lys	Phe	Tyr	Gly	Glu	Asn	Leu	Lys	Thr					
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 Thr Pro Glu Phe Ile Ala Phe Phe Ser Gly Ile Ile Ile Phe Val Asp  
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 Thr Ser Ala Pro Val Cys Leu Leu Val Pro Ile Ser Ser Trp Gly Ala  
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 Pro Ser Met Arg Lys Tyr Gln Asn Ile Gly Val Lys Asp Phe Tyr Ser  
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090901 062901

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 Ile Ser Leu Ser Val Lys His Thr Asp Asn  
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 Val Ile Ser Leu Arg Lys Glu Asn Gly Val Arg Thr Leu Ile Ser Leu  
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 Gly Ile Leu Leu Ser Val Leu Ser Gly Asp Asp Leu Lys Leu Tyr Ser  
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 Lys Leu Ser Val Tyr Ser Ala Gly Ser Gly Met Ile Gly Ile Asp Ile  
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 Asp Lys Arg Thr Phe Tyr Lys Arg Ala Phe Ala Phe Thr Met Lys Ser  
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 Leu Thr Ser Lys His Met Lys Gly Pro Leu Glu Asn Arg His His His  
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 Ser Phe Thr Lys Asn Tyr Glu Lys Ala Val Asn Gly Cys Gln Lys Tyr  
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 Phe His Ile Lys Leu Pro Glu Gly Ala Pro Ser Asn Phe Lys Ser Gly  
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-104-



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Ala Asp Phe Phe Lys Asn Phe Lys Ile Asn Lys Leu Arg Thr Ala Pro	
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Ser Lys Glu Glu Gln Pro Ser His Trp Val Lys Cys Pro Lys Cys Tyr	
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Ala Leu Met Tyr His Lys Glu Val Phe Ser Lys Tyr Ser Val Cys Leu	
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Lys Cys His Tyr His Phe Arg Met Lys Ala Ala Glu Arg Ile Glu Phe	
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Leu Cys Asp Val Gly Ser Phe Glu Glu Phe Asp Lys His Leu Arg Pro	
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Asn Asp Pro Leu Asn Phe Val Asp Lys Glu Ser Tyr Lys Gln Arg Ile	
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Lys Lys Tyr Glu Lys Arg Thr Asn Arg Pro Ser Ser Val Ile Ser Gly	
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Glu Ala Lys Ile Asn Arg Met Pro Leu Gln Ile Val Val Phe Asp Phe	
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Arg Ala Ile Asn Arg Ala Val Ala Lys Arg Glu Ala Leu Leu Ile Val	
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Gln Met Ala Lys Thr Ser Ala Ala Leu Asn Arg Leu Ser Glu Ala Lys	
180 185 190 195	
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Asp	Leu	Pro	Glu	Gly	Phe	Gln	Thr	Ala	Glu	Phe	Leu	Leu	Glu	His	Gly		
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Leu	Ile	Asp	Met	Ile	Val	His	Arg	Lys	Asp	Leu	Lys	Lys	Thr	Leu	Ser		
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gat	ctc	atc	gct	atg	atg	acg	cat	aag	act	tca	aag	att	ttt				976
Asp	Leu	Ile	Ala	Met	Met	Thr	His	Lys	Thr	Ser	Lys	Ile	Phe				
				280					285								
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gtagtgaaaa	atctatc																1053

<210> 98  
 <211> 289  
 <212> PRT  
 <213> Helicobacter pylori

<400> 98

Met	Gly	Phe	Ala	Asp	Phe	Phe	Lys	Asn	Phe	Lys	Ile	Asn	Lys	Leu	Arg		
1				5					10					15			
Thr	Ala	Pro	Ser	Lys	Glu	Glu	Gln	Pro	Ser	His	Trp	Val	Lys	Cys	Pro		
			20					25					30				
Lys	Cys	Tyr	Ala	Leu	Met	Tyr	His	Lys	Glu	Val	Phe	Ser	Lys	Tyr	Ser		
		35					40					45					
Val	Cys	Leu	Lys	Cys	His	Tyr	His	Phe	Arg	Met	Lys	Ala	Ala	Glu	Arg		
	50					55				60							
Ile	Glu	Phe	Leu	Cys	Asp	Val	Gly	Ser	Phe	Glu	Glu	Phe	Asp	Lys	His		
65				70					75					80			
Leu	Arg	Pro	Asn	Asp	Pro	Leu	Asn	Phe	Val	Asp	Lys	Glu	Ser	Tyr	Lys		
			85					90					95				
Gln	Arg	Ile	Lys	Lys	Tyr	Glu	Lys	Arg	Thr	Asn	Arg	Pro	Ser	Ser	Val		
			100					105					110				
Ile	Ser	Gly	Glu	Ala	Lys	Ile	Asn	Arg	Met	Pro	Leu	Gln	Ile	Val	Val		
		115					120					125					
Phe	Asp	Phe	Ser	Phe	Met	Gly	Gly	Ser	Leu	Gly	Ser	Val	Glu	Gly	Glu		
	130					135					140						
Lys	Ile	Val	Arg	Ala	Ile	Asn	Arg	Ala	Val	Ala	Lys	Arg	Glu	Ala	Leu		
					150				155					160			
Leu	Ile	Val	Ser	Ala	Ser	Gly	Gly	Ala	Arg	Met	Gln	Glu	Ser	Thr	Tyr		
				165				170						175			
Ser	Leu	Met	Gln	Met	Ala	Lys	Thr	Ser	Ala	Ala	Leu	Asn	Arg	Leu	Ser		
		180						185					190				
Glu	Ala	Lys	Leu	Pro	Phe	Ile	Ser	Leu	Leu	Ser	Asp	Pro	Thr	Tyr	Gly		
		195				200						205					
Gly	Val	Ser	Ala	Ser	Phe	Ala	Phe	Leu	Gly	Asp	Leu	Ile	Ile	Ala	Glu		

210	215	220
Pro Gly Ala Met Ile Gly	Phe Ala Gly Pro Arg Val	Ile Lys Gln Thr
225	230	235
Ile Gly Ala Asp Leu Pro	Glu Gly Phe Gln Thr	Ala Glu Phe Leu Leu
245	250	255
Glu His Gly Leu Ile Asp	Met Ile Val His Arg	Lys Asp Leu Lys Lys
260	265	270
Thr Leu Ser Asp Leu Ile	Ala Met Met Thr His	Lys Thr Ser Lys Ile
275	280	285
Phe		

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 <212> DNA  
 <213> Helicobacter pylori

<220>  
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gcttataata aacaaaatta gcttaagagt agtg atg caa ggg ttt ctt tta caa	115
Met Gln Gly Phe Leu Leu Gln	
1 5	
aca caa agc ata aga gat gaa gat ttg atc gtg cgc gtt tta acc aaa	163
Thr Gln Ser Ile Arg Asp Glu Asp Leu Ile Val Arg Val Leu Thr Lys	
10 15 20	
aac cag ctc aaa acc ctc tat cgt ttc tat ggc aaa cgc cat agc gtg	211
Asn Gln Leu Lys Thr Leu Tyr Arg Phe Tyr Gly Lys Arg His Ser Val	
25 30 35	
ctg aat gtg ggg cgt aaa att gat ttt gaa gaa gaa aac gat gat aag	259
Leu Asn Val Gly Arg Lys Ile Asp Phe Glu Glu Glu Asn Asp Asp Lys	
40 45 50 55	
ttt tta ccc aag tta agg aat att ttg cat tta ggc tat att tgg gaa	307
Phe Leu Pro Lys Leu Arg Asn Ile Leu His Leu Gly Tyr Ile Trp Glu	
60 65 70	
aga gaa atg gag cgc ttg ttt ttt tgg caa cgc ttt tgc gct ctc ttg	355
Arg Glu Met Glu Arg Leu Phe Phe Trp Gln Arg Phe Cys Ala Leu Leu	
75 80 85	
ttt agg cat tta gaa ggc gtg cat tct tta gat agc gtc tat ttt gac	403
Phe Arg His Leu Glu Gly Val His Ser Leu Asp Ser Val Tyr Phe Asp	
90 95 100	
act tta gat gat ggg gct aac aaa ctc gcc aaa cag cac ccc tta aga	451
Thr Leu Asp Asp Gly Ala Asn Lys Leu Ala Lys Gln His Pro Leu Arg	
105 110 115	
gtg att tta gaa atg tat gca acg ctt ttg aat ttt gaa ggg cgc ttg	499
Val Ile Leu Glu Met Tyr Ala Thr Leu Leu Asn Phe Glu Gly Arg Leu	
120 125 130 135	

TO6290"EF65860



caa agt tac aat tct tgt ttt tta tgc gat gca aaa tta gag cgt tct	547
Gln Ser Tyr Asn Ser Cys Phe Leu Cys Asp Ala Lys Leu Glu Arg Ser	
140 145 150	
gtc gct tta gcg caa ggg ttt att cta gcg cac ccc tct tgt ttg aaa	595
Val Ala Leu Ala Gln Gly Phe Ile Leu Ala His Pro Ser Cys Leu Lys	
155 160 165	
gct aaa agc cta aat tta gaa aaa atc caa gct ttt ttt cgc act caa	643
Ala Lys Ser Leu Asn Leu Glu Lys Ile Gln Ala Phe Phe Arg Thr Gln	
170 175 180	
agc acg att gat tta gaa aca gaa gaa gta gaa gaa tta tgg cgc acg	691
Ser Thr Ile Asp Leu Glu Thr Glu Glu Val Glu Glu Leu Trp Arg Thr	
185 190 195	
ctg aat tta ggg ttt tgaaaggta aaaatgaaat ttaaattttt gaatatggat	746
Leu Asn Leu Gly Phe	
200	
aatgaaagcg gttttatttt gattgaaaaa gaattgaaac gattaaacat tctcgctcaa	806
gtca	810

<210> 100  
 <211> 204  
 <212> PRT  
 <213> Helicobacter pylori

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20 25 30	
Tyr Gly Lys Arg His Ser Val Leu Asn Val Gly Arg Lys Ile Asp Phe	
35 40 45	
Glu Glu Glu Asn Asp Asp Lys Phe Leu Pro Lys Leu Arg Asn Ile Leu	
50 55 60	
His Leu Gly Tyr Ile Trp Glu Arg Glu Met Glu Arg Leu Phe Phe Trp	
65 70 75 80	
Gln Arg Phe Cys Ala Leu Leu Phe Arg His Leu Glu Gly Val His Ser	
85 90 95	
Leu Asp Ser Val Tyr Phe Asp Thr Leu Asp Asp Gly Ala Asn Lys Leu	
100 105 110	
Ala Lys Gln His Pro Leu Arg Val Ile Leu Glu Met Tyr Ala Thr Leu	
115 120 125	
Leu Asn Phe Glu Gly Arg Leu Gln Ser Tyr Asn Ser Cys Phe Leu Cys	
130 135 140	
Asp Ala Lys Leu Glu Arg Ser Val Ala Leu Ala Gln Gly Phe Ile Leu	
145 150 155 160	
Ala His Pro Ser Cys Leu Lys Ala Lys Ser Leu Asn Leu Glu Lys Ile	
165 170 175	
Gln Ala Phe Phe Arg Thr Gln Ser Thr Ile Asp Leu Glu Thr Glu Glu	
180 185 190	
Val Glu Glu Leu Trp Arg Thr Leu Asn Leu Gly Phe	
195 200	

<210> 101  
 <211> 999  
 <212> DNA

**SECRET**

<221> CDS

<222> (76) ... (927)

<400> 101

-110-

tta atg gta atg tgg gct aaa aaa cac acc aaa acg cat ggg ttg ctg 735  
 Leu Met Val Met Trp Ala Lys Lys His Thr Lys Thr His Gly Leu Leu  
 205 210 215 220

att gtg gtt tat ggt ttg ggg tat tcc ttg atg cgc ttt att gcg gaa 783  
 Ile Val Val Tyr Gly Leu Gly Tyr Ser Leu Met Arg Phe Ile Ala Glu  
 225 230 235

ttt tac aga gag ccg gac agc caa atg ggg gtt tat ttt tta aat ttg 831  
 Phe Tyr Arg Glu Pro Asp Ser Gln Met Gly Val Tyr Phe Leu Asn Leu  
 240 245 250

agc atg ggg cag att tta agc tta ttt atg gta att gtt tcg tta ggg 879  
 Ser Met Gly Gln Ile Leu Ser Leu Phe Met Val Ile Val Ser Leu Gly  
 255 260 265

att tta ttg tat gct aca aaa aat tct aaa aaa ata aag gaa aat caa 927  
 Ile Leu Leu Tyr Ala Thr Lys Asn Ser Lys Lys Ile Lys Glu Asn Gln  
 270 275 280

tgaaattttt ggatcaagaa aaaagaagac aattattaaa cgagcgccat tcttgcaaga 987  
 tgtttgatag cc 999

<210> 102  
 <211> 284  
 <212> PRT  
 <213> Helicobacter pylori

<400> 102  
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 20 25 30  
 Ala Ile Val Thr Ala Phe Tyr Met Ala Leu Arg Met Ile Gln Lys Asp  
 35 40 45  
 Pro Lys Arg Phe Pro Ile Glu Arg Lys Glu Phe Glu Ser Tyr Phe Leu  
 50 55 60  
 Trp Ala Glu Leu Gly Ile Val Leu Gly Ala Arg Ile Gly Tyr Ile Leu  
 65 70 75 80  
 Ile Tyr Glu Pro Asn Ser Gly Tyr Tyr Leu Thr His Phe Trp Gln Ile  
 85 90 95  
 Phe Asn Pro Phe Asp Ser His Gly Asn Phe Val Gly Ile Arg Gly Met  
 100 105 110  
 Ser Tyr His Gly Gly Leu Val Gly Phe Leu Ile Ala Ser Tyr Leu Tyr  
 115 120 125  
 Ser Arg Lys Asp Leu Lys Lys Leu Leu Ile Tyr Leu Asp Leu Ile Ala  
 130 135 140  
 Ile Ser Leu Pro Leu Gly Tyr Val Phe Gly Arg Ile Gly Asn Phe Leu  
 145 150 155 160  
 Asn Gln Glu Leu Val Gly Arg Ile Val Pro Lys Asp Ser His Leu Gly  
 165 170 175  
 Gln Ile Ile Gly Ile Met Val Asp Asn Glu Leu Arg Tyr Pro Ser Gln  
 180 185 190  
 Leu Ile Glu Ala Phe Leu Glu Gly Val Ile Val Phe Leu Met Val Met  
 195 200 205  
 Trp Ala Lys Lys His Thr Lys Thr His Gly Leu Leu Ile Val Val Tyr  
 210 215 220  
 Gly Leu Gly Tyr Ser Leu Met Arg Phe Ile Ala Glu Phe Tyr Arg Glu



att cct gta gag atc act tac ggc tta gaa aga tta gcg atg tat gtg 592  
Ile Pro Val Glu Ile Thr Tyr Gly Leu Glu Arg Leu Ala Met Tyr Val  
155 160 165

caa aaa gtg gaa aat atc cta gag att gaa tgg gct aaa aaa aat cat 640  
Gln Lys Val Glu Asn Ile Leu Glu Ile Glu Trp Ala Lys Lys Asn His  
170 175 180 185

gac agc gtg aat tac gca caa gtg cat ttg gaa agc gaa tac gaa ttc 688  
Asp Ser Val Asn Tyr Ala Gln Val His Leu Glu Ser Glu Tyr Glu Phe  
190 195 200

agc aag tat cat ttt gaa aca gcg agc gtg aaa cgg cta tta gaa atg 736  
Ser Lys Tyr His Phe Glu Thr Ala Ser Val Lys Arg Leu Leu Glu Met  
205 210 215

ttt aaa aac gct caa gcc gaa gcc ttg cat tgc ttg gaa aac aag ctc 784  
Phe Lys Asn Ala Gln Ala Glu Ala Leu His Cys Leu Glu Asn Lys Leu  
220 225 230

ccc ttg ccg gct tat gat ttt gtg atg tta tgc tcg cat ttt ttc aat 832  
Pro Leu Pro Ala Tyr Asp Phe Val Met Leu Cys Ser His Phe Phe Asn  
235 240 245

att tta gac gcc aga aaa gcg att tcg gtg gct gaa agg caa aat tat 880  
Ile Leu Asp Ala Arg Lys Ala Ile Ser Val Ala Glu Arg Gln Asn Tyr  
250 255 260 265

att tta caa atc agg gat tta gcc aaa ggg tgt gcg ctt ctt tat aaa 928  
Ile Leu Gln Ile Arg Asp Leu Ala Lys Gly Cys Ala Leu Leu Tyr Lys  
270 275 280

gaa caa gaa gaa gag agg gaa gag cgt tta aaa aac gct tta aca aag 976  
Glu Gln Glu Glu Glu Arg Glu Glu Arg Leu Lys Asn Ala Leu Thr Lys  
285 290 295

gct gaa aat ggc gtt agt taaggaagtg ttggtagttt tgaatcgcct 1024  
Ala Glu Asn Gly Val Ser  
300

ttcgccctttt gaactccaag aatcatggga taatagcggg ttgaatgtgg ggagtgaaaa 1084  
tagtgaattt agcgagattg 1104

<210> 104  
<211> 303  
<212> PRT  
<213> Helicobacter pylori

<400> 104  
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20 25 30  
Gly Thr Phe His Pro Ala Thr Leu Leu Arg Ser Leu Asp Lys Lys Pro  
35 40 45  
Trp Asn Val Ala Tyr Val Ala Pro Ser Arg Arg Pro Thr Asp Gly Arg  
50 55 60  
Tyr Gly Glu Asn Pro Asn Arg Leu Gly Ser Tyr Tyr Gln Phe Gln Val  
65 70 75 80

Val Ile Lys Pro Ser Pro Ser Asn Ile Gln Glu Leu Tyr Leu Lys Ser  
85 90 95  
Leu Glu Val Leu Gly Ile Asn Leu Asn Glu His Asp Ile Arg Phe Val  
100 105 110  
Glu Asp Asn Trp Glu Ser Pro Thr Leu Gly Ala Trp Gly Leu Gly Trp  
115 120 125  
Glu Val Trp Leu Asp Gly Met Glu Val Thr Gln Phe Thr Tyr Phe Gln  
130 135 140  
Gln Val Gly Gly Ile Ala Cys Ser Pro Ile Pro Val Glu Ile Thr Tyr  
145 150 155 160  
Gly Leu Glu Arg Leu Ala Met Tyr Val Gln Lys Val Glu Asn Ile Leu  
165 170 175  
Glu Ile Glu Trp Ala Lys Lys Asn His Asp Ser Val Asn Tyr Ala Gln  
180 185 190  
Val His Leu Glu Ser Glu Tyr Glu Phe Ser Lys Tyr His Phe Glu Thr  
195 200 205  
Ala Ser Val Lys Arg Leu Leu Glu Met Phe Lys Asn Ala Gln Ala Glu  
210 215 220  
Ala Leu His Cys Leu Glu Asn Lys Leu Pro Leu Pro Ala Tyr Asp Phe  
225 230 235 240  
Val Met Leu Cys Ser His Phe Phe Asn Ile Leu Asp Ala Arg Lys Ala  
245 250 255  
Ile Ser Val Ala Glu Arg Gln Asn Tyr Ile Leu Gln Ile Arg Asp Leu  
260 265 270  
Ala Lys Gly Cys Ala Leu Leu Tyr Lys Glu Gln Glu Glu Glu Arg Glu  
275 280 285  
Glu Arg Leu Lys Asn Ala Leu Thr Lys Ala Glu Asn Gly Val Ser  
290 295 300

<210> 105  
<211> 1620  
<212> DNA  
<213> Helicobacter pylori  
<220>  
<221> CDS  
<222> (66)...(1538)

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taaaa atg gcg caa aaa act ctt ttg att atc act gat ggc att ggg tat 110  
Met Ala Gln Lys Thr Leu Leu Ile Ile Thr Asp Gly Ile Gly Tyr  
1 5 10 15  
cgt aaa gat agc gat cat aac gct ttc ttc cat gcc aaa aaa ccc act 158  
Arg Lys Asp Ser Asp His Asn Ala Phe Phe His Ala Lys Lys Pro Thr  
20 25 30  
tat gat ttg atg ttt aaa acc ttg cct tat agc ctg att gat acg cat 206  
Tyr Asp Leu Met Phe Lys Thr Leu Pro Tyr Ser Leu Ile Asp Thr His  
35 40 45  
ggc ttg agc gtg ggc tta cct aag ggg caa atg gga aat tct gaa gtg 254  
Gly Leu Ser Val Gly Leu Pro Lys Gly Gln Met Gly Asn Ser Glu Val  
50 55 60  
ggg cat atg tgt att ggg gct ggt agg gtg ctc tat cag gat tta gtc 302  
Gly His Met Cys Ile Gly Ala Gly Arg Val Leu Tyr Gln Asp Leu Val  
65 70 75

aaa Lys 80	att Ile	tct Ser	tta Leu	agc Ser	ctt Leu 85	caa Gln	aac Asn	gat Asp	gaa Glu	tta Leu 90	aaa Lys	aac Asn	aac Asn	ccc Pro	gct Ala 95	350
ttt Phe	tta Leu	aac Asn	acg Thr	atc Ile 100	caa Gln	aaa Lys	agc Ser	cct Pro	gtg Val 105	gtg Val	cat His	ctt Leu	atg Met	ggt Gly 110	tta Leu	398
atg Met	agc Ser	gat Asp	gga Gly 115	ggc Gly	gtg Val	cat His	tca Ser	cac His	att Ile	gag Glu	cat His	ttt Phe	atc Ile	gct Ala 125	ctg Leu	446
gct Ala	tta Leu	gag Glu 130	tgt Cys	gaa Glu	aaa Lys	tcc Ser	cat His	aaa Lys	aaa Lys	gtc Val	tgt Cys	ctg Leu	cat His	tta Leu	atc Ile	494
acc Thr	gat Asp 145	ggg Gly	cgc Arg	gat Asp	gtc Val	gct Ala 150	cct Pro	aaa Lys	agc Ser	gct Ala	tta Leu 155	act Thr	tat Tyr	tta Leu	aaa Lys	542
caa Gln 160	atg Met	caa Gln	aat Asn	atc Ile	tgc Cys 165	aat Asn	gaa Glu	agc Ser	att Ile	caa Gln 170	atc Ile	gct Ala	acc Thr	ata Ile	agc Ser 175	590
ggc Gly	cgt Arg	ttt Phe	tat Tyr	gcc Ala 180	atg Met	gat Asp	agg Arg	gat Asp	aag Lys 185	cgc Arg	ttt Phe	gaa Glu	agg Arg	att Ile 190	gag Glu	638
ctt Leu	gcg Ala	tat Tyr	cat His 195	agc Ser	tta Leu	atg Met	ggg Gly	ctt Leu 200	aat Asn	cac His	acg Thr	cct Pro	tta Leu 205	agc Ser	cct Pro	686
agc Ser	gag Glu	tat Tyr 210	atc Ile	caa Gln	agc Ser	cag Gln	tat Tyr 215	gat Asp	aaa Lys	aat Asn	atc Ile	acc Thr 220	gat Asp	gaa Glu	ttt Phe	734
atc Ile	atg Met 225	ccc Pro	gct Ala	tgt Cys	ttt Phe	aaa Lys 230	aat Asn	tat Tyr	tgc Cys	ggc Gly	atg Met 235	caa Gln	gat Asp	gat Asp	gag Glu	782
agt Ser 240	ttt Phe	att Ile	ttt Phe	atc Ile	aat Asn 245	ttc Phe	agg Arg	aat Asn	gat Asp	agg Arg	gct Ala	aga Arg	gaa Glu	atc Ile	gtg Val 255	830
agc Ser	gct Ala	tta Leu	ggc Gly	caa Gln 260	aaa Lys	caa Gln	ttc Phe	agt Ser	ggc Gly 265	ttt Phe	aag Lys	cgc Arg	caa Gln	gtt Val 270	ttt Phe	878
aaa Lys	aaa Lys	ctc Leu	cat His 275	atc Ile	gct Ala	acc Thr	atg Met	acg Thr	cct Pro	tat Tyr	gat Asp	aac Asn	act Thr 285	ttc Phe	ccc Pro	926
tac Tyr	cct Pro	gtt Val 290	tta Leu	ttc Phe	ccc Pro	aaa Lys	gaa Glu 295	agc Ser	gtt Val	caa Gln	aac Asn	acg Thr 300	ctc Leu	gct Ala	gaa Glu	974
gtg Val	gtc Val	tct Ser	caa Gln	cac His	aac Asn	ctg Leu	acc Thr	caa Gln	agc Ser	cat His	atc Ile	gct Ala	gaa Glu	act Thr	gaa Glu	1022

305	310	315	
aaa tac gcg cat gta acc ttt ttc atc aat ggc gga gtg gag acg cct Lys Tyr Ala His Val Thr Phe Phe Ile Asn Gly Gly Val Glu Thr Pro 320 325 330 335			1070
ttt aaa aat gaa aac cgg gtg ctt atc caa agc cct aaa gtt acc act Phe Lys Asn Glu Asn Arg Val Leu Ile Gln Ser Pro Lys Val Thr Thr 340 345 350			1118
tat gac tta aag cct gaa atg agc gct aaa gaa gta acc ctt gcg gtg Tyr Asp Leu Lys Pro Glu Met Ser Ala Lys Glu Val Thr Leu Ala Val 355 360 365			1166
tta gag caa atg aaa cta ggc acg gat ttg atc att gtg aat ttt gct Leu Glu Gln Met Lys Leu Gly Thr Asp Leu Ile Ile Val Asn Phe Ala 370 375 380			1214
aat ggc gat atg gta ggg cat acg ggg aat ttt gaa gcg agc gtc aaa Asn Gly Asp Met Val Gly His Thr Gly Asn Phe Glu Ala Ser Val Lys 385 390 395			1262
gcg gtg gaa gca gtg gat gca tgt tta ggg gaa atc ctt tca ctg gct Ala Val Glu Ala Val Asp Ala Cys Leu Gly Glu Ile Leu Ser Leu Ala 400 405 410 415			1310
aaa aaa ttg gat tac gcc atg ctt tta acc agc gat cat ggg aat tgc Lys Lys Leu Asp Tyr Ala Met Leu Leu Thr Ser Asp His Gly Asn Cys 420 425 430			1358
gag cgc atg aaa gac gaa aac caa aac ccc tta acc aac cac acc gcc Glu Arg Met Lys Asp Glu Asn Gln Asn Pro Leu Thr Asn His Thr Ala 435 440 445			1406
ggg agc gtg tat tgc ttt gtt tta ggg gat gga gtc aaa tcc ata aaa Gly Ser Val Tyr Cys Phe Val Leu Gly Asp Gly Val Lys Ser Ile Lys 450 455 460			1454
aac gga gcc tta aac aat atc gct agc agc gtg tta aaa ctc atg ggc Asn Gly Ala Leu Asn Asn Ile Ala Ser Ser Val Leu Lys Leu Met Gly 465 470 475			1502
ctt aaa gcc cca gca acg atg gac gaa ccc cta ttt taaactaaag Leu Lys Ala Pro Ala Thr Met Asp Glu Pro Leu Phe 480 485 490			1548
gaaaagaatg caaattgatg acgcattatt gcaacgcttg gaaaaattga gcatgctaga gattaaagat ga			1608 1620
<210> 106			
<211> 491			
<212> PRT			
<213> Helicobacter pylori			
<400> 106			
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Lys Asp Ser Asp His Asn Ala Phe Phe His Ala Lys Lys Pro Thr Tyr 20 25 30			



Asp	Leu	Met	Phe	Lys	Thr	Leu	Pro	Tyr	Ser	Leu	Ile	Asp	Thr	His	Gly
		35					40					45			
Leu	Ser	Val	Gly	Leu	Pro	Lys	Gly	Gln	Met	Gly	Asn	Ser	Glu	Val	Gly
		50				55					60				
His	Met	Cys	Ile	Gly	Ala	Gly	Arg	Val	Leu	Tyr	Gln	Asp	Leu	Val	Lys
65					70					75					80
Ile	Ser	Leu	Ser	Leu	Gln	Asn	Asp	Glu	Leu	Lys	Asn	Asn	Pro	Ala	Phe
				85					90					95	
Leu	Asn	Thr	Ile	Gln	Lys	Ser	Pro	Val	Val	His	Leu	Met	Gly	Leu	Met
			100					105					110		
Ser	Asp	Gly	Gly	Val	His	Ser	His	Ile	Glu	His	Phe	Ile	Ala	Leu	Ala
		115					120					125			
Leu	Glu	Cys	Glu	Lys	Ser	His	Lys	Lys	Val	Cys	Leu	His	Leu	Ile	Thr
		130				135					140				
Asp	Gly	Arg	Asp	Val	Ala	Pro	Lys	Ser	Ala	Leu	Thr	Tyr	Leu	Lys	Gln
145					150					155					160
Met	Gln	Asn	Ile	Cys	Asn	Glu	Ser	Ile	Gln	Ile	Ala	Thr	Ile	Ser	Gly
				165					170					175	
Arg	Phe	Tyr	Ala	Met	Asp	Arg	Asp	Lys	Arg	Phe	Glu	Arg	Ile	Glu	Leu
			180					185					190		
Ala	Tyr	His	Ser	Leu	Met	Gly	Leu	Asn	His	Thr	Pro	Leu	Ser	Pro	Ser
		195					200					205			
Glu	Tyr	Ile	Gln	Ser	Gln	Tyr	Asp	Lys	Asn	Ile	Thr	Asp	Glu	Phe	Ile
		210				215					220				
Met	Pro	Ala	Cys	Phe	Lys	Asn	Tyr	Cys	Gly	Met	Gln	Asp	Asp	Glu	Ser
225					230					235					240
Phe	Ile	Phe	Ile	Asn	Phe	Arg	Asn	Asp	Arg	Ala	Arg	Glu	Ile	Val	Ser
				245					250					255	
Ala	Leu	Gly	Gln	Lys	Gln	Phe	Ser	Gly	Phe	Lys	Arg	Gln	Val	Phe	Lys
			260					265					270		
Lys	Leu	His	Ile	Ala	Thr	Met	Thr	Pro	Tyr	Asp	Asn	Thr	Phe	Pro	Tyr
		275					280					285			
Pro	Val	Leu	Phe	Pro	Lys	Glu	Ser	Val	Gln	Asn	Thr	Leu	Ala	Glu	Val
		290				295					300				
Val	Ser	Gln	His	Asn	Leu	Thr	Gln	Ser	His	Ile	Ala	Glu	Thr	Glu	Lys
305					310					315					320
Tyr	Ala	His	Val	Thr	Phe	Phe	Ile	Asn	Gly	Gly	Val	Glu	Thr	Pro	Phe
				325					330					335	
Lys	Asn	Glu	Asn	Arg	Val	Leu	Ile	Gln	Ser	Pro	Lys	Val	Thr	Thr	Tyr
			340					345					350		
Asp	Leu	Lys	Pro	Glu	Met	Ser	Ala	Lys	Glu	Val	Thr	Leu	Ala	Val	Leu
		355					360					365			
Glu	Gln	Met	Lys	Leu	Gly	Thr	Asp	Leu	Ile	Ile	Val	Asn	Phe	Ala	Asn
		370				375					380				
Gly	Asp	Met	Val	Gly	His										

<210> 107  
 <211> 1440  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
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 <222> (72)...(1379)

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           Met Asn Phe Gln Glu Asn Leu Ala Ala Leu Asp Leu Glu  
           1                          5                          10

tat ctt tgg cac cct tgt tgc caa atg caa gag cat caa aat ttc ccc 158  
 Tyr Leu Trp His Pro Cys Ser Gln Met Gln Glu His Gln Asn Phe Pro  
       15                          20                          25

att atc ccc att aaa aag gct caa ggg att tac ctc tat gat ttt aat 206  
 Ile Ile Pro Ile Lys Lys Ala Gln Gly Ile Tyr Leu Tyr Asp Phe Asn  
       30                          35                          40                          45

gat aac gct tac atg gat ttg atc agc tca tgg tgg gtg aat ctt ttt 254  
 Asp Asn Ala Tyr Met Asp Leu Ile Ser Ser Trp Trp Val Asn Leu Phe  
                           50                          55                          60

ggg cat aat aac gcc tac atc agc cag caa ctc aaa aat caa att gat 302  
 Gly His Asn Asn Ala Tyr Ile Ser Gln Gln Leu Lys Asn Gln Ile Asp  
                           65                          70                          75

gat tta gag cat gtc ctt ttg gct tct ttt agc cat aag ccc att atc 350  
 Asp Leu Glu His Val Leu Leu Ala Ser Phe Ser His Lys Pro Ile Ile  
                           80                          85                          90

acg ctc tct caa agg ctt tgc cag ctc act cat atg gat aaa tgc ttt 398  
 Thr Leu Ser Gln Arg Leu Cys Gln Leu Thr His Met Asp Lys Cys Phe  
                           95                          100                          105

tat gcg gat aac ggc tca tct tgt gtt gaa atc gct ttg aaa atg agc 446  
 Tyr Ala Asp Asn Gly Ser Ser Cys Val Glu Ile Ala Leu Lys Met Ser  
 110                          115                          120                          125

tat cac gcc cat ttt tta aag aat caa acg cgc cgc aaa aag ctt ttt 494  
 Tyr His Ala His Phe Leu Lys Asn Gln Thr Arg Arg Lys Lys Leu Phe  
                           130                          135                          140

tta tgc ctc tct aat tcc tat cat ggc gag act ttg gga gcg tta agc 542  
 Leu Ser Leu Ser Asn Ser Tyr His Gly Glu Thr Leu Gly Ala Leu Ser  
                           145                          150                          155

gtg ggc gat gtg aaa ctt tat aaa gac act tac acc cct tta ttg ctc 590  
 Val Gly Asp Val Lys Leu Tyr Lys Asp Thr Tyr Thr Pro Leu Leu Leu  
                           160                          165                          170

aaa aat ctc acc aca cct gtg cct aaa aac gac cat gaa ata gaa aat 638  
 Lys Asn Leu Thr Thr Pro Val Pro Lys Asn Asp His Glu Ile Glu Asn  
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006690-ET656860

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190 195 200 205	
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Cys Ala Phe Ile Ala Glu Pro Leu Leu Gln Cys Ala Gly Asn Met His	
210 215 220	
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Ile Tyr Ser Ala Arg Tyr Leu Lys Gln Ala Val Leu Leu Cys Lys Gln	
225 230 235	
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Lys Asn Ile His Ile Ile Phe Asp Glu Ile Ala Thr Gly Phe Gly Arg	
240 245 250	
aca ggg agc atg ttt gct tat gaa caa tgc gaa att aag ccg gat ttt	878
Thr Gly Ser Met Phe Ala Tyr Glu Gln Cys Glu Ile Lys Pro Asp Phe	
255 260 265	
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Leu Cys Leu Ser Lys Gly Ile Ser Gly Gly Tyr Leu Pro Leu Ser Ala	
270 275 280 285	
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Leu Leu Thr His Asn Glu Ile Tyr Asn Gln Phe Tyr Ala Pro Tyr Glu	
290 295 300	
gaa aat aaa gcg ttt ttg cat tcg cac agc tac aca gga aac gct ttg	1022
Glu Asn Lys Ala Phe Leu His Ser His Ser Tyr Thr Gly Asn Ala Leu	
305 310 315	
gca tgc gca tgc gcg aac gct acg ctg gat att ttt gaa aaa gaa aat	1070
Ala Cys Ala Cys Ala Asn Ala Thr Leu Asp Ile Phe Glu Lys Glu Asn	
320 325 330	
gtt att gaa aag aac aag gct tta agc ggg ttt att ttt aat acg ctc	1118
Val Ile Glu Lys Asn Lys Ala Leu Ser Gly Phe Ile Phe Asn Thr Leu	
335 340 345	
caa aac gca tta aaa ccc ttg atg gag caa caa gtg gtg tct gat tta	1166
Gln Asn Ala Leu Lys Pro Leu Met Glu Gln Gln Val Val Ser Asp Leu	
350 355 360 365	
agg cat ttg ggc atg gtc ttt gcc ttt gaa gtc ttt att caa acc aaa	1214
Arg His Leu Gly Met Val Phe Ala Phe Glu Val Phe Ile Gln Thr Lys	
370 375 380	
gag cgt ttg agt ttg gcg gtt ttt aaa aaa act cta aaa aaa ggc ctg	1262
Glu Arg Leu Ser Leu Ala Val Phe Lys Lys Thr Leu Lys Lys Gly Leu	
385 390 395	
tta tta cgc cct tta aac aac acc att tac ctc atg ccc cct tac att	1310
Leu Leu Arg Pro Leu Asn Asn Thr Ile Tyr Leu Met Pro Pro Tyr Ile	
400 405 410	
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Ile Thr His Glu Glu Val Lys Lys Ala Val Ala Gly Leu Val Glu Ile	
415 420 425	



Gly Met Val Phe Ala Phe Glu Val Phe Ile Gln Thr Lys Glu Arg Leu  
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 Ser Leu Ala Val Phe Lys Lys Thr Leu Lys Lys Gly Leu Leu Leu Arg  
 385 390 395 400  
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 Met Gly Lys Met Lys Gln Glu Thr Ala Ile  
 1 5 10  
 gac tat gaa aaa tta gcg aat cat tgg aat aat aat gat gaa aac agc 159  
 Asp Tyr Glu Lys Leu Ala Asn His Trp Asn Asn Asn Asp Glu Asn Ser  
 15 20 25  
 gaa gca cta aac gct ttt gca gac gct tac ctt tat aaa cat gag aaa 207  
 Glu Ala Leu Asn Ala Phe Ala Asp Ala Tyr Leu Tyr Lys His Glu Lys  
 30 35 40  
 aag agt caa aag att cgg gca ata gag ata agt tct cta aac aaa gcc 255  
 Lys Ser Gln Lys Ile Arg Ala Ile Glu Ile Ser Ser Leu Asn Lys Ala  
 45 50 55  
 tgc atg gga gaa ttt tac cac aaa aac cca aaa tta ttt taataacgat 304  
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 60 65 70  
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 <212> PRT  
 <213> Helicobacter pylori

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 Ala Asp Ala Tyr Leu Tyr Lys His Glu Lys Lys Ser Gln Lys Ile Arg  
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 Arg His Arg Asn Arg Ala Arg Cys Thr Arg Lys Gln Ala Arg Asn Asn  
 1 5 10 15

aag agt ttt agg cat gaa aac tat ttt tat aaa gtt ttg ggt agt gca 157  
 Lys Ser Phe Arg His Glu Asn Tyr Phe Tyr Lys Val Leu Gly Ser Ala  
 20 25 30

act tct caa ata gaa agt ttg aaa aaa aga gaa aat gcc cta ttt gat 205  
 Thr Ser Gln Ile Glu Ser Leu Lys Lys Arg Glu Asn Ala Leu Phe Asp  
 35 40 45

cat tta gat agt cta aaa agt tta tta gaa aaa aca cat tgg gaa aaa 253  
 His Leu Asp Ser Leu Lys Ser Leu Leu Glu Lys Thr His Trp Glu Lys  
 50 55 60

gaa aaa ttc acg ccc cca ata aat gaa aaa gaa ctt aat agg caa ctt 301  
 Glu Lys Phe Thr Pro Ile Asn Glu Lys Glu Leu Asn Arg Gln Leu  
 65 70 75 80

aaa gaa gtg aga tgg ttc aat aaa gaa act cca act tct aaa aac act 349  
 Lys Glu Val Arg Trp Phe Asn Lys Glu Thr Pro Thr Ser Lys Asn Thr  
 85 90 95

tat aag aaa att caa aaa tta gct gtt tat aaa agc cct tta ata aaa 397  
 Tyr Lys Lys Ile Gln Lys Leu Ala Val Tyr Lys Ser Pro Leu Ile Lys  
 100 105 110

gat tat ctt tat acc att aaa aaa ctt ttt gcc aca caa aaa aag att 445  
 Asp Tyr Leu Tyr Thr Ile Lys Lys Leu Phe Ala Thr Gln Lys Lys Ile  
 115 120 125

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 130 135 140

ttt agc aaa gat tta gaa act gat tta tcc cat tca aaa aaa cgc ttt 541  
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 145 150 155 160

gaa ctt tac act aga cta aag agc atg agc aaa gtt ttt ata agc aaa 589  
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 165 170 175

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106290"ET65860

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aag ttt ttt aaa gat agt gct tta ctt gtt aat att gct agg ttt gaa Lys Phe Phe Lys Asp Ser Ala Leu Leu Val Asn Ile Ala Arg Phe Glu 225 230 235 240			781
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ctt gaa gag gaa aat tat tgt ttt gct aag aaa cga aaa gaa ttc tta Leu Glu Glu Glu Asn Tyr Cys Phe Ala Lys Lys Arg Lys Glu Phe Leu 275 280 285			925
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gct aat gaa aat gat ttg ccc att tat gaa aga ggg caa agg gat aaa Ala Asn Glu Asn Asp Leu Pro Ile Tyr Glu Arg Gly Gln Arg Asp Lys 305 310 315 320			1021
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caa tgc ttt aaa acc tta ttg aaa agt gca agt ata gct tta gaa aac Gln Cys Phe Lys Thr Leu Leu Lys Ser Ala Ser Ile Ala Leu Glu Asn 340 345 350			1117
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Thr	Ser	Gln 35	Ile	Glu	Ser	Leu	Lys 40	Lys	Arg	Glu	Asn	Ala 45	Leu	Phe	Asp
His	Leu 50	Asp	Ser	Leu	Lys	Ser 55	Leu	Leu	Glu	Lys	Thr 60	His	Trp	Glu	Lys
Glu 65	Lys	Phe	Thr	Pro	Pro 70	Ile	Asn	Glu	Lys	Glu 75	Leu	Asn	Arg	Gln	Leu 80
Lys	Glu	Val	Arg	Trp 85	Phe	Asn	Lys	Glu	Thr 90	Pro	Thr	Ser	Lys	Asn 95	Thr
Tyr	Lys	Lys	Ile 100	Gln	Lys	Leu	Ala	Val 105	Tyr	Lys	Ser	Pro	Leu	Ile	Lys
Asp	Tyr	Leu 115	Tyr	Thr	Ile	Lys	Lys 120	Leu	Phe	Ala	Thr	Gln 125	Lys	Lys	Ile
Ile	Asp 130	Leu	Glu	Lys	Asn	Tyr 135	Lys	Asp	Leu	Arg	Ala 140	Leu	Lys	Glu	Glu
Phe 145	Ser	Lys	Asp	Leu	Glu 150	Thr	Asp	Leu	Ser	His 155	Ser	Lys	Lys	Arg	Phe 160
Glu	Leu	Tyr	Thr	Arg 165	Leu	Lys	Ser	Met	Ser 170	Lys	Val	Phe	Ile	Ser 175	Lys
Ser	Ile	Val	Lys 180	Asn	Leu	Glu	Lys	Ile 185	Ala	Leu	Asp	Phe	Lys 190	Ser	Asp
Arg	His	Ser 195	Ile	Ser	Gln	Arg	Ala 200	Phe	Glu	Phe	Phe	Lys 205	Tyr	Met	Asn
Tyr	Gln 210	Asn	Leu	Ser	Leu	Thr 215	Asp	Lys	Gly	Asn	Met 220	Phe	Leu	Val	Ala
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Ala 305	Asn	Glu	Asn	Asp	Leu 310	Pro	Ile	Tyr	Glu	Arg 315	Gly	Gln	Arg	Asp	Lys
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<213> Helicobacter pylori



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-125-







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1709

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His Leu Leu Met Ile Ala Phe Gly Gly Ala Ile Gly Thr Gly Leu Phe  
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130 135 140  
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gag Glu 245	tta Leu	aga Arg	aat Asn	cta Leu	atc Ile	ggc Gly 250	tcc Ser	atg Met	cta Leu	ccc Pro	aat Asn 255	caa Gln	aga Arg	gta Val	acc Thr	1006
tta Leu 260	aaa Lys	gtc Val	att Ile	aga Arg	gac Asp 265	aaa Lys	aaa Lys	gaa Glu	cgc Arg	gct Ala 270	ttc Phe	acc Thr	ctc Leu	act Thr	cta Leu 275	1054
gct Ala	gaa Glu	agg Arg	aaa Lys	aac Asn 280	cct Pro	aac Asn	aaa Lys	aaa Lys	gaa Glu 285	acc Thr	att Ile	tct Ser	gct Ala	caa Gln 290	aac Asn	1102
ggc Gly	gcg Ala	caa Gln	ggc Gly 295	caa Gln	ttg Leu	aac Asn	ggg Gly 300	ctt Leu	caa Gln	gta Val	gaa Glu	gat Asp	tta Leu 305	act Thr	caa Gln	1150
gaa Glu	acc Thr 310	aaa Lys	agg Arg	tct Ser	atg Met	cgt Arg	ttg Leu 315	agc Ser	gat Asp	gat Asp	gtt Val	caa Gln 320	ggg Gly	gtt Val	tta Leu	1198
gtc Val 325	tct Ser	caa Gln	gtg Val	aat Asn	gaa Glu	aat Asn 330	tcc Ser	cca Pro	gca Ala	gag Glu 335	caa Gln	gcc Ala	gga Gly	ttt Phe	agg Arg	1246

caa ggt aac att atc aca aaa att gaa gag gtt gaa gtt aaa agc gtt	1294
Gln Gly Asn Ile Ile Thr Lys Ile Glu Glu Val Glu Val Lys Ser Val	
340 345 350 355	
gcg gat ttt aac cat gct tta gaa aag tat aaa ggc aaa ccc aaa cga	1342
Ala Asp Phe Asn His Ala Leu Glu Lys Tyr Lys Gly Lys Pro Lys Arg	
360 365 370	
ttc tta gtt tta gac ttg aat caa ggt tat agg atc att ttg gtg aaa	1390
Phe Leu Val Leu Asp Leu Asn Gln Gly Tyr Arg Ile Ile Leu Val Lys	
375 380 385	
tgataggggt gggtcgtag tcgcatgtct ttgattagag tgaatgggga agctttttaa	1450
ctctcttttag aaagttaga agaagaccct ttgaaacta aagaaacgct agaaacgctt	1510
atcaaacaaa cgagcgttg	1529

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 <211> 387  
 <212> FRT  
 <213> Helicobacter pylori

<400> 120	
Met Ile Pro Lys Glu Arg Met Glu Arg Ala Leu Gly Ser Gly Val Ile	
1 5 10 15	
Ile Ser Lys Asp Gly Tyr Ile Val Thr Asn Asn His Val Ile Asp Gly	
20 25 30	
Ala Asp Lys Ile Lys Val Thr Ile Pro Gly Ser Asn Lys Glu Tyr Ser	
35 40 45	
Ala Thr Leu Val Gly Thr Asp Ser Glu Ser Asp Leu Ala Val Ile Arg	
50 55 60	
Ile Thr Lys Asp Asn Leu Pro Thr Ile Lys Phe Ser Asp Ser Asn Asp	
65 70 75 80	
Ile Ser Val Gly Asp Leu Val Phe Ala Ile Gly Asn Pro Phe Gly Val	
85 90 95	
Gly Glu Ser Val Thr Gln Gly Ile Val Ser Ala Leu Asn Lys Ser Gly	
100 105 110	
Ile Gly Ile Asn Ser Tyr Glu Asn Phe Ile Gln Thr Asp Ala Ser Ile	
115 120 125	
Asn Pro Gly Asn Ser Gly Gly Ala Leu Ile Asp Ser Arg Gly Gly Leu	
130 135 140	
Val Gly Ile Asn Thr Ala Ile Ile Ser Lys Thr Gly Gly Asn His Gly	
145 150 155 160	
Ile Gly Phe Ala Ile Pro Ser Asn Met Val Lys Asp Thr Val Thr Gln	
165 170 175	
Leu Ile Lys Thr Gly Lys Ile Glu Arg Gly Tyr Leu Gly Val Gly Leu	
180 185 190	
Gln Asp Leu Ser Gly Asp Leu Gln Asn Ser Tyr Asp Asn Lys Glu Gly	
195 200 205	
Ala Val Val Ile Ser Val Glu Lys Asp Ser Pro Ala Lys Lys Ala Gly	
210 215 220	
Ile Leu Val Trp Asp Leu Ile Thr Glu Val Asn Gly Lys Lys Val Lys	
225 230 235 240	
Asn Thr Asn Glu Leu Arg Asn Leu Ile Gly Ser Met Leu Pro Asn Gln	
245 250 255	
Arg Val Thr Leu Lys Val Ile Arg Asp Lys Lys Glu Arg Ala Phe Thr	
260 265 270	
Leu Thr Leu Ala Glu Arg Lys Asn Pro Asn Lys Lys Glu Thr Ile Ser	
275 280 285	

Ala Gln Asn Gly Ala Gln Gly Gln Leu Asn Gly Leu Gln Val Glu Asp  
 290 295 300  
 Leu Thr Gln Glu Thr Lys Arg Ser Met Arg Leu Ser Asp Asp Val Gln  
 305 310 315 320  
 Gly Val Leu Val Ser Gln Val Asn Glu Asn Ser Pro Ala Glu Gln Ala  
 325 330 335  
 Gly Phe Arg Gln Gly Asn Ile Ile Thr Lys Ile Glu Glu Val Glu Val  
 340 345 350  
 Lys Ser Val Ala Asp Phe Asn His Ala Leu Glu Lys Tyr Lys Gly Lys  
 355 360 365  
 Pro Lys Arg Phe Leu Val Leu Asp Leu Asn Gln Gly Tyr Arg Ile Ile  
 370 375 380  
 Leu Val Lys  
 385

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 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (39)...(902)

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 Met Ser Lys Ser Leu Tyr  
 1 5  
 caa act tta aat gtg agc gaa aac gcc agc caa gat gaa atc aaa aaa 104  
 Gln Thr Leu Asn Val Ser Glu Asn Ala Ser Gln Asp Glu Ile Lys Lys  
 10 15 20  
 tcc tac cgc cgt tta gcc cga caa tac cac ccg gat ttg aat aaa acc 152  
 Ser Tyr Arg Arg Leu Ala Arg Gln Tyr His Pro Asp Leu Asn Lys Thr  
 25 30 35  
 aaa gaa gcc gaa gag aaa ttc aaa gaa atc aac gcc gct tat gaa att 200  
 Lys Glu Ala Glu Glu Lys Phe Lys Glu Ile Asn Ala Ala Tyr Glu Ile  
 40 45 50  
 ttg agc gat gaa gaa aaa cgc cgc caa tac gat cag ttt ggc gat aac 248  
 Leu Ser Asp Glu Glu Lys Arg Arg Gln Tyr Asp Gln Phe Gly Asp Asn  
 55 60 65 70  
 atg ttt ggc ggg cag aat ttc agc gat ttt gcc aga agc cgt ggt cct 296  
 Met Phe Gly Gly Gln Asn Phe Ser Asp Phe Ala Arg Ser Arg Gly Pro  
 75 80 85  
 agt gaa gat tta gac gat att tta agc tct att ttt ggg aaa gga ggc 344  
 Ser Glu Asp Leu Asp Asp Ile Leu Ser Ser Ile Phe Gly Lys Gly Gly  
 90 95 100  
 ttt tcg caa aga ttt tct caa aac tcg caa ggc ttt tct ggc ttt aat 392  
 Phe Ser Gln Arg Phe Ser Gln Asn Ser Gln Gly Phe Ser Gly Phe Asn  
 105 110 115  
 ttt tcc aat ttc gcc cct gaa aat tta gac ata acc gcc gct tta aat 440  
 Phe Ser Asn Phe Ala Pro Glu Asn Leu Asp Ile Thr Ala Ala Leu Asn



Asp Gln Phe Gly Asp Asn Met Phe Gly Gly Gln Asn Phe Ser Asp Phe  
65 70 75 80  
Ala Arg Ser Arg Gly Pro Ser Glu Asp Leu Asp Asp Ile Leu Ser Ser  
85 90 95  
Ile Phe Gly Lys Gly Gly Phe Ser Gln Arg Phe Ser Gln Asn Ser Gln  
100 105 110  
Gly Phe Ser Gly Phe Asn Phe Ser Asn Phe Ala Pro Glu Asn Leu Asp  
115 120 125  
Ile Thr Ala Ala Leu Asn Val Ser Val Leu Asp Thr Leu Leu Gly Asn  
130 135 140  
Lys Lys Gln Val Ser Ile Asn Asn Glu Thr Phe Ser Leu Lys Ile Pro  
145 150 155 160  
Ile Gly Val Glu Glu Gly Glu Lys Ile Arg Val Arg Asn Lys Gly Lys  
165 170 175  
Thr Gly Arg Thr Thr Arg Gly Asp Leu Leu Leu Glu Ile His Ile Glu  
180 185 190  
Glu Asp Glu Met Tyr Arg Arg Glu Lys Asp Asp Ile Thr Gln Ile Phe  
195 200 205  
Asp Leu Pro Leu Lys Thr Ala Leu Phe Gly Gly Lys Ile Glu Ile Ala  
210 215 220  
Thr Trp His Lys Thr Leu Thr Leu Thr Ile Pro Pro Asn Thr Lys Ala  
225 230 235 240  
Met Gln Lys Phe Arg Ile Lys Glu Lys Gly Ile Lys Asn Arg Lys Thr  
245 250 255  
Ser His Val Gly Asp Leu Tyr Leu Gln Ala Arg Leu Ile Leu Pro Lys  
260 265 270  
Thr Glu Thr Leu Ser Asn Glu Leu Lys Ala Leu Leu Glu Lys Glu Leu  
275 280 285

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<212> DNA  
<213> Helicobacter pylori  
<220>  
<221> CDS  
<222> (113)...(1285)

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cgaaaaattt aaacaccctt acgaattttt acgaattgat tttattttaa aa atg agc 118  
Met Ser  
1  
ctg act tcg ctt tta aac cca aaa agc cta gaa gat ttt tta ggc caa 166  
Leu Thr Ser Leu Leu Asn Pro Lys Ser Leu Glu Asp Phe Leu Gly Gln  
5 10 15  
gag cat tta gta ggg aaa gac gcc ccc tta ttt aaa gcc cta caa tcc 214  
Glu His Leu Val Gly Lys Asp Ala Pro Leu Phe Lys Ala Leu Gln Ser  
20 25 30  
aaa cac ttc ccc cat gcc ttt ttc tat ggc cct cct ggc gtg ggt aaa 262  
Lys His Phe Pro His Ala Phe Phe Tyr Gly Pro Pro Gly Val Gly Lys  
35 40 45 50  
aca agc ctg gct caa atc atc gcc tat atg cta gag cgc ccc att ctt 310  
Thr Ser Leu Ala Gln Ile Ile Ala Tyr Met Leu Glu Arg Pro Ile Leu  
55 60 65

tta	ttc	aat	gcg	acg	gat	ttt	aaa	tta	gag	gat	ttg	cgc	ctt	aag	ctt	358
Leu	Phe	Asn	Ala	Thr	Asp	Phe	Lys	Leu	Glu	Asp	Leu	Arg	Leu	Lys	Leu	
			70				75			80						
aaa	aat	tac	caa	aat	acc	ctt	tta	aaa	ccc	gtt	gtt	ttt	att	gat	gaa	406
Lys	Asn	Tyr	Gln	Asn	Thr	Leu	Leu	Lys	Pro	Val	Val	Phe	Ile	Asp	Glu	
			85				90			95						
acc	cac	aga	ttg	aat	aaa	acc	caa	caa	gaa	ttt	tta	ctc	ccc	att	atg	454
Thr	His	Arg	Leu	Asn	Lys	Thr	Gln	Gln	Glu	Phe	Leu	Leu	Pro	Ile	Met	
			100				105			110						
gaa	aaa	gat	cac	gct	tta	att	tta	ggg	gct	agc	acg	caa	gat	cct	aat	502
Glu	Lys	Asp	His	Ala	Leu	Ile	Leu	Gly	Ala	Ser	Thr	Gln	Asp	Pro	Asn	
			115	120						125			130			
tac	agc	cta	agc	cat	gcg	atc	cga	tca	aga	agt	ttt	att	ttt	gaa	tta	550
Tyr	Ser	Leu	Ser	His	Ala	Ile	Arg	Ser	Arg	Ser	Phe	Ile	Phe	Glu	Leu	
			135				140						145			
acc	ccc	cta	aac	aag	agc	gat	tta	gac	agg	ctt	tgc	gct	aaa	gct	tta	598
Thr	Pro	Leu	Asn	Lys	Ser	Asp	Leu	Asp	Arg	Leu	Cys	Ala	Lys	Ala	Leu	
			150				155						160			
aca	ttg	ctc	aaa	aaa	caa	ata	gag	cct	ggc	gct	aaa	acc	tat	ctt	tta	646
Thr	Leu	Leu	Lys	Lys	Gln	Ile	Glu	Pro	Gly	Ala	Lys	Thr	Tyr	Leu	Leu	
			165				170			175						
aac	aac	agc	gct	ggc	gac	gct	aga	gcg	tta	tta	aac	ctt	tta	gat	ttg	694
Asn	Asn	Ser	Ala	Gly	Asp	Ala	Arg	Ala	Leu	Leu	Asn	Leu	Leu	Asp	Leu	
			180	185						190						
agc	gct	aaa	ata	gaa	gat	cct	atc	act	tta	aaa	acg	cta	caa	tcc	tta	742
Ser	Ala	Lys	Ile	Glu	Asp	Pro	Ile	Thr	Leu	Lys	Thr	Leu	Gln	Ser	Leu	
			195	200						205			210			
cgg	cct	cat	agc	cta	aat	gat	gga	tct	tat	agc	gat	gat	acg	cat	tat	790
Arg	Pro	His	Ser	Leu	Asn	Asp	Gly	Ser	Tyr	Ser	Asp	Asp	Thr	His	Tyr	
			215				220						225			
aac	ctt	act	agc	gcg	tta	atc	aaa	tct	tta	aga	ggg	agc	gat	gaa	aac	838
Asn	Leu	Thr	Ser	Ala	Leu	Ile	Lys	Ser	Leu	Arg	Gly	Ser	Asp	Glu	Asn	
			230				235						240			
gct	tcc	atc	tat	tat	ctg	gcg	cgc	ttg	att	gct	ggc	ggg	gaa	aac	ccg	886
Ala	Ser	Ile	Tyr	Tyr	Leu	Ala	Arg	Leu	Ile	Ala	Gly	Gly	Glu	Asn	Pro	
			245				250			255						
gaa	ttt	atc	gcc	aga	agg	ctg	gtg	att	ttt	gcg	agc	gaa	gat	att	ggt	934
Glu	Phe	Ile	Ala	Arg	Arg	Leu	Val	Ile	Phe	Ala	Ser	Glu	Asp	Ile	Gly	
			260	265						270						
aac	gct	aac	ccg	aac	gcc	ctt	aat	tta	gcc	gct	tct	tgt	ttg	ttt	gca	982
Asn	Ala	Asn	Pro	Asn	Ala	Leu	Asn	Leu	Ala	Ala	Ser	Cys	Leu	Phe	Ala	
			275	280						285			290			
gtc	aaa	caa	atc	ggc	tac	cct	gaa	gcg	cgc	atc	att	tta	agc	caa	tgc	1030
Val	Lys	Gln	Ile	Gly	Tyr	Pro	Glu	Ala								

[illegible]

195	200	205
Ser Leu Arg Pro His Ser	Leu Asn Asp Gly Ser Tyr	Ser Asp Asp Thr
210	215	220
His Tyr Asn Leu Thr Ser	Ala Leu Ile Lys Ser	Leu Arg Gly Ser Asp
225	230	235
Glu Asn Ala Ser Ile Tyr	Tyr Leu Ala Arg Leu	Ile Ala Gly Gly Glu
245	250	255
Asn Pro Glu Phe Ile Ala	Arg Arg Leu Val Ile Phe	Ala Ser Glu Asp
260	265	270
Ile Gly Asn Ala Asn Pro	Asn Ala Leu Asn Leu	Ala Ala Ser Cys Leu
275	280	285
Phe Ala Val Lys Gln Ile	Gly Tyr Pro Glu Ala	Arg Ile Ile Leu Ser
290	295	300
Gln Cys Val Ile Tyr Leu	Ala Cys Ser Pro Lys	Ser Asn Thr Ala Tyr
305	310	315
Arg Ala Ile Asn Gln Ala	Leu Asp Cys Val Gln	Lys Gly Ser Leu Tyr
325	330	335
Pro Ile Pro Lys His Leu	Leu Pro Asn Ala Lys	Asp Tyr Leu Tyr Pro
340	345	350
His Asp Tyr Asn Gly Tyr	Val Lys Gln Asp Tyr	Leu Glu Lys Pro Leu
355	360	365
Asp Leu Val Ser Ser Gln	Gly Ile Gly Phe Glu	Lys Thr Leu Leu Glu
370	375	380
Trp Leu Asp Lys Ile Arg	Asn	
385	390	

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 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (76)...(759)

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aagaaacttt taacaaacaa ttcaagggat ttggcgattt tgggtcttaa aaaatatgct	60
attttatggt cttta atg ggg ttt tat gca gga ttg aac gcg ctt gat tat	111
Met Gly Phe Tyr Ala Gly Leu Asn Ala Leu Asp Tyr	
1 5 10	
gac acc ata gac cca aaa tac tac aag tat atc aag tat tat aaa gcc	159
Asp Thr Ile Asp Pro Lys Tyr Tyr Lys Tyr Ile Lys Tyr Tyr Lys Ala	
15 20 25	
tat gag gat aaa gaa gtt gaa gaa ttg atc aga gac tta aaa agg gcg	207
Tyr Glu Asp Lys Glu Val Glu Glu Leu Ile Arg Asp Leu Lys Arg Ala	
30 35 40	
aac gct aaa agc ggg ctt att tta ggg atc aat acc ggg ttt ttt tac	255
Asn Ala Lys Ser Gly Leu Ile Leu Gly Ile Asn Thr Gly Phe Phe Tyr	
45 50 55 60	
aat cat gaa atc atg gtt aga act aat agc tct agc atc acg ggg aat	303
Asn His Glu Ile Met Val Arg Thr Asn Ser Ser Ser Ile Thr Gly Asn	
65 70 75	
att tta aat tat ttg ttc gct tac ggc ttg cgt ttt ggc tat caa act	351
Ile Leu Asn Tyr Leu Phe Ala Tyr Gly Leu Arg Phe Gly Tyr Gln Thr	



80	85	90	
ttc agg ccg tcg ttt ttt gcg cgc ttg gtc aag cca aat atc att ggc			399
Phe Arg Pro Ser Phe Phe Ala Arg Leu Val Lys Pro Asn Ile Ile Gly			
95	100	105	
agg cgc att tat atc caa tat tat gga gga gct cct aaa aaa gcg ggc			447
Arg Arg Ile Tyr Ile Gln Tyr Tyr Gly Gly Ala Pro Lys Lys Ala Gly			
110	115	120	
ttt ggg gat gta ggg ttt caa tcg gtt atg ctg aat ggg gat ttt tta			495
Phe Gly Asp Val Gly Phe Gln Ser Val Met Leu Asn Gly Asp Phe Leu			
125	130	135	140
ttg gat ttt cct ttg cct ttt gtg ggg aaa tac ctt tat atg ggg ggt			543
Leu Asp Phe Pro Leu Pro Phe Val Gly Lys Tyr Leu Tyr Met Gly Gly			
145	150	155	
tat atg ggt tta ggt ttg ggg gtt gta gcg cat ggg gtg aat tac acg			591
Tyr Met Gly Leu Gly Leu Gly Val Val Ala His Gly Val Asn Tyr Thr			
160	165	170	
gcg gaa tgg ggg atg tct ttt aac gca gga ttg gct cta acg gta tta			639
Ala Glu Trp Gly Met Ser Phe Asn Ala Gly Leu Ala Leu Thr Val Leu			
175	180	185	
gaa aaa aac cgc att gaa ttt gga ttt aaa att ttg aat aat ttc cct			687
Glu Lys Asn Arg Ile Glu Phe Gly Phe Lys Ile Leu Asn Asn Phe Pro			
190	195	200	
ttt ttg caa tct aat tct tca aaa gag act tgg tgg gga gct atg gca			735
Phe Leu Gln Ser Asn Ser Ser Lys Glu Thr Trp Trp Gly Ala Met Ala			
205	210	215	220
aac att ggg tat caa tat gtg ttc taaaaaata agaaatctca ttttatgctt			789
Asn Ile Gly Tyr Gln Tyr Val Phe			
225			
tggttttatg ttgggcttgc acgctgaaga aaatacgact gaaggaaata tgactgaaga			849
aaatatctct aaagacgctc			869
<210> 126			
<211> 228			
<212> PRT			
<213> Helicobacter pylori			
<400> 126			
Met Gly Phe Tyr Ala Gly Leu Asn Ala Leu Asp Tyr Asp Thr Ile Asp			
1 5 10 15			
Pro Lys Tyr Tyr Lys Tyr Ile Lys Tyr Tyr Lys Ala Tyr Glu Asp Lys			
20 25 30			
Glu Val Glu Glu Leu Ile Arg Asp Leu Lys Arg Ala Asn Ala Lys Ser			
35 40 45			
Gly Leu Ile Leu Gly Ile Asn Thr Gly Phe Phe Tyr Asn His Glu Ile			
50 55 60			
Met Val Arg Thr Asn Ser Ser Ile Thr Gly Asn Ile Leu Asn Tyr			
65 70 75 80			
Leu Phe Ala Tyr Gly Leu Arg Phe Gly Tyr Gln Thr Phe Arg Pro Ser			
85 90 95			

Phe Phe Ala Arg Leu Val Lys Pro Asn Ile Ile Gly Arg Arg Ile Tyr  
 100 105 110  
 Ile Gln Tyr Tyr Gly Gly Ala Pro Lys Lys Ala Gly Phe Gly Asp Val  
 115 120 125  
 Gly Phe Gln Ser Val Met Leu Asn Gly Asp Phe Leu Leu Asp Phe Pro  
 130 135 140  
 Leu Pro Phe Val Gly Lys Tyr Leu Tyr Met Gly Gly Tyr Met Gly Leu  
 145 150 155 160  
 Gly Leu Gly Val Val Ala His Gly Val Asn Tyr Thr Ala Glu Trp Gly  
 165 170 175  
 Met Ser Phe Asn Ala Gly Leu Ala Leu Thr Val Leu Glu Lys Asn Arg  
 180 185 190  
 Ile Glu Phe Gly Phe Lys Ile Leu Asn Asn Phe Pro Phe Leu Gln Ser  
 195 200 205  
 Asn Ser Ser Lys Glu Thr Trp Trp Gly Ala Met Ala Asn Ile Gly Tyr  
 210 215 220  
 Gln Tyr Val Phe  
 225

<210> 127  
 <211> 1171  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (89)...(1096)

<400> 127  
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 tccctaacga attagaaagt tatcatta atg aaa gaa cgg ata gtc aat tta 112  
 Met Lys Glu Arg Ile Val Asn Leu  
 1 5  
 gaa act ttg gat ttt gaa att tct caa gaa gtg agt ttg cgc cct agt 160  
 Glu Thr Leu Asp Phe Glu Ile Ser Gln Glu Val Ser Leu Arg Pro Ser  
 10 15 20  
 ctt tgg gaa gat ttt atc ggt caa gaa aag att aaa agc aat ttg caa 208  
 Leu Trp Glu Asp Phe Ile Gly Gln Glu Lys Ile Lys Ser Asn Leu Gln  
 25 30 35 40  
 att tct att tgc gcg gct aaa aaa cgc caa gaa agt ttg gat cac atg 256  
 Ile Ser Ile Cys Ala Ala Lys Lys Arg Gln Glu Ser Leu Asp His Met  
 45 50 55  
 ctt ttt ttt ggc ccg ccc ggt ttg ggt aaa act tca atc agc cat atc 304  
 Leu Phe Phe Gly Pro Pro Gly Leu Gly Lys Thr Ser Ile Ser His Ile  
 60 65 70  
 atc gct aaa gaa atg gaa acc aat atc aag atc acc gcc gct ccc atg 352  
 Ile Ala Lys Glu Met Glu Thr Asn Ile Lys Ile Thr Ala Ala Pro Met  
 75 80 85  
 ata gaa aaa agc ggt gat tta gcc gcc att ttg acc aat ttg caa gct 400  
 Ile Glu Lys Ser Gly Asp Leu Ala Ala Ile Leu Thr Asn Leu Gln Ala  
 90 95 100  
 aaa gac att ctt ttt att gat gaa atc cac cgg ctc agc cca gcg att 448

Lys	Asp	Ile	Leu	Phe	Ile	Asp	Glu	Ile	His	Arg	Leu	Ser	Pro	Ala	Ile		
105					110					115					120		
gaa	gag	gtt	tta	tac	ccg	gcg	atg	gaa	gat	ttt	agg	ttg	gat	att	atc		496
Glu	Glu	Val	Leu	Tyr	Pro	Ala	Met	Glu	Asp	Phe	Arg	Leu	Asp	Ile	Ile		
				125					130					135			
ata	ggc	tca	ggc	cca	gcg	gct	caa	acc	att	aaa	att	gat	tta	ccc	cct		544
Ile	Gly	Ser	Gly	Pro	Ala	Ala	Gln	Thr	Ile	Lys	Ile	Asp	Leu	Pro	Pro		
			140					145					150				
ttc	act	ctc	atc	ggc	gct	acc	acc	aga	gcc	gga	atg	ctc	tct	aac	ccc		592
Phe	Thr		Leu	Ile	Gly	Ala	Thr	Arg	Ala	Gly	Met	Leu	Ser	Asn	Pro		
			155					160					165				
tta	aga	gac	aga	ttt	ggc	atg	agt	ttt	aga	atg	caa	ttt	tat	aac	cct		640
Leu	Arg	Asp	Arg	Phe	Gly	Met	Ser	Phe	Arg	Met	Gln	Phe	Tyr	Asn	Pro		
	170					175					180						
agc	gaa	ctg	gcc	ctc	atc	att	aaa	aaa	gct	gcc	gtt	aaa	ctc	aac	caa		688
Ser	Glu	Leu	Ala	Leu	Ile	Ile	Lys	Lys	Ala	Ala	Val	Lys	Leu	Asn	Gln		
185					190					195				200			
gac	atc	aaa	caa	gaa	agt	gct	gat	gaa	atc	gct	aaa	agg	agt	aga	ggc		736
Asp	Ile	Lys	Gln	Glu	Ser	Ala	Asp	Glu	Ile	Ala	Lys	Arg	Ser	Arg	Gly		
			205						210					215			
acg	cca	agg	atc	gct	tta	agg	ctt	tta	aaa	agg	gtg	cgc	gat	ttt	gcg		784
Thr	Pro	Arg	Ile	Ala	Leu	Arg	Leu	Leu	Lys	Arg	Val	Arg	Asp	Phe	Ala		
			220					225					230				
cta	gtc	aaa	aat	tca	agc	ttg	atg	gat	tta	aac	atc	act	ttg	cat	gct		832
Leu	Val	Lys	Asn	Ser	Ser	Leu	Met	Asp	Leu	Asn	Ile	Thr	Leu	His	Ala		
		235					240					245					
ttg	aat	gaa	tta	ggc	gtg	aat	gaa	tta	ggc	ttt	gat	gaa	gcg	gat	ttg		880
Leu	Asn	Glu	Leu	Gly	Val	Asn	Glu	Leu	Gly	Phe	Asp	Glu	Ala	Asp	Leu		
	250					255					260						
gcg	tat	tta	tct	ttg	ttg	gct	aac	gct	caa	gga	aag	ccg	gtg	ggt	ttg		928
Ala	Tyr	Leu	Ser	Leu	Leu	Ala	Asn	Ala	Gln	Gly	Lys	Pro	Val	Gly	Leu		
265				270					275					280			
aac	acg	att	gca	gca	tct	atg	aga	gaa	gat	gaa	ggc	acg	att	gaa	gac		976
Asn	Thr	Ile	Ala	Ala	Ser	Met	Arg	Glu	Asp	Glu	Gly	Thr	Ile	Glu	Asp		
			285					290						295			
gtg	att	gag	cct	ttt	tta	ctc	gct	aat	ggg	tat	tta	gag	cgc	acc	gct		1024
Val	Ile	Glu	Pro	Phe	Leu	Leu	Ala	Asn	Gly	Tyr	Leu	Glu	Arg	Thr	Ala		
			300					305					310				
aaa	ggc	aga	atc	gcc	acg	cct	aaa	acc	cat	gag	ctc	tta	aaa	atc	ccc		1072
Lys	Gly	Arg	Ile	Ala	Thr	Pro	Lys	Thr	His	Glu	Leu	Leu	Lys	Ile	Pro		
		315					320					325					
act	tta	aac	ccc	caa	act	tta	ttt	taat	ctt	ggt	tagaa	agaaa	attac	actac			1126
Thr	Leu	Asn	Pro	Gln	Thr	Leu	Phe										
	330					335											



<400> 129  
agttttccaat gaagaagcct taaacaaaga agttttcaagc gatgaatccc ctaaagaagt 60  
ccaattagca accgataaca acaccaaaga acacgacaaa gaaaaagaga atg ttt 116  
Met Phe  
1

gaa gat tta aaa ccg cat tta cag gaa tta aga aag cgt ttg atg gtt 164  
Glu Asp Leu Lys Pro His Leu Gln Glu Leu Arg Lys Arg Leu Met Val  
5 10 15

tct gta gga acg att cta gtg gcg ttt ttg ggg tgc ttt cat ttt tgg 212  
Ser Val Gly Thr Ile Leu Val Ala Phe Leu Gly Cys Phe His Phe Trp  
20 25 30

aaa agt att ttt gaa ttt gtt aaa aat tcc tat aaa ggc acg ctc att 260  
Lys Ser Ile Phe Glu Phe Val Lys Asn Ser Tyr Lys Gly Thr Leu Ile  
35 40 45 50

cag ctc tcc cct att gaa ggg gtc atg gta gcg gtt aaa atc agt ttt 308  
Gln Leu Ser Pro Ile Glu Gly Val Met Val Ala Val Lys Ile Ser Phe  
55 60 65

tca gcc gct atc gtc att tcc atg ccc att att ttt tgg caa tta tgg 356  
Ser Ala Ala Ile Val Ile Ser Met Pro Ile Ile Phe Trp Gln Leu Trp  
70 75 80

ctc ttt atc gct cca ggg ctt tac aag aat gaa aaa aaa gtg att ttg 404  
Leu Phe Ile Ala Pro Gly Leu Tyr Lys Asn Glu Lys Lys Val Ile Leu  
85 90 95

cct ttt gtg ttt ttt ggg agt ggg atg ttt ttg att ggg gcg gcg ttt 452  
Pro Phe Val Phe Phe Gly Ser Gly Met Phe Leu Ile Gly Ala Ala Phe  
100 105 110

tct tat tat gtg gtg ttc cct ttc att att gaa tac tta gcc act ttt 500  
Ser Tyr Tyr Val Val Phe Pro Phe Ile Ile Glu Tyr Leu Ala Thr Phe  
115 120 125 130

ggg agc gat gtg ttt gcg gct aat att tct gcg tcc agt tac gtg agc 548  
Gly Ser Asp Val Phe Ala Ala Asn Ile Ser Ala Ser Ser Tyr Val Ser  
135 140 145

ttt ttc acg cgc ttg att tta ggc ttt ggc gtg gcg ttt gaa ttg cct 596  
Phe Phe Thr Arg Leu Ile Leu Gly Phe Gly Val Ala Phe Glu Leu Pro  
150 155 160

gtt ttg gcg tat ttt ttg gct aaa gtg ggc ttg att act gat gcg agc 644  
Val Leu Ala Tyr Phe Leu Ala Lys Val Gly Leu Ile Thr Asp Ala Ser  
165 170 175

ttg aaa gcg tat ttt aaa tac gct att gta gtg att ttt att gta gca 692  
Leu Lys Ala Tyr Phe Lys Tyr Ala Ile Val Val Ile Phe Ile Val Ala  
180 185 190

gcc att atc act ccc cct gat gtg gtg agt caa atc ttt atg gcg ttg 740  
Ala Ile Ile Thr Pro Asp Val Val Ser Gln Ile Phe Met Ala Leu  
195 200 205 210

ccc tta gtg ggg ctt tat ggg ctt tct att tta atc gcc aaa atg gtc 788

Pro Leu Val Gly Leu Tyr Gly Leu Ser Ile Leu Ile Ala Lys Met Val  
215 220 225

aat ccg gct ccc aaa gat aac gaa aat aac aac gaa aat aat aac gaa 836  
Asn Pro Ala Pro Lys Asp Asn Glu Asn Asn Glu Asn Asn Asn Glu  
230 235 240

aat aac acc aaa gag aat aca aag agc gag tcg tagttgaaag aatttgattt 889  
Asn Asn Thr Lys Glu Asn Thr Lys Ser Glu Ser  
245 250

agaaaagctat gattattatt tgcctaagga attgatcgca agctaccccg ttttgcccaa 949  
agaaaaggct aaattactcg tctatgaaag gcgttcgcaa 989

<210> 130  
<211> 253  
<212> PRT  
<213> Helicobacter pylori

<400> 130

Met Phe Glu Asp Leu Lys Pro His Leu Gln Glu Leu Arg Lys Arg Leu  
1 5 10 15  
Met Val Ser Val Gly Thr Ile Leu Val Ala Phe Leu Gly Cys Phe His  
20 25 30  
Phe Trp Lys Ser Ile Phe Glu Phe Val Lys Asn Ser Tyr Lys Gly Thr  
35 40 45  
Leu Ile Gln Leu Ser Pro Ile Glu Gly Val Met Val Ala Val Lys Ile  
50 55 60  
Ser Phe Ser Ala Ala Ile Val Ile Ser Met Pro Ile Ile Phe Trp Gln  
65 70 75 80  
Leu Trp Leu Phe Ile Ala Pro Gly Leu Tyr Lys Asn Glu Lys Lys Val  
85 90 95  
Ile Leu Pro Phe Val Phe Phe Gly Ser Gly Met Phe Leu Ile Gly Ala  
100 105 110  
Ala Phe Ser Tyr Tyr Val Val Phe Pro Phe Ile Ile Glu Tyr Leu Ala  
115 120 125  
Thr Phe Gly Ser Asp Val Phe Ala Ala Asn Ile Ser Ala Ser Ser Tyr  
130 135 140  
Val Ser Phe Phe Thr Arg Leu Ile Leu Gly Phe Gly Val Ala Phe Glu  
145 150 155 160  
Leu Pro Val Leu Ala Tyr Phe Leu Ala Lys Val Gly Leu Ile Thr Asp  
165 170 175  
Ala Ser Leu Lys Ala Tyr Phe Lys Tyr Ala Ile Val Val Ile Phe Ile  
180 185 190  
Val Ala Ala Ile Ile Thr Pro Pro Asp Val Val Ser Gln Ile Phe Met  
195 200 205  
Ala Leu Pro Leu Val Gly Leu Tyr Gly Leu Ser Ile Leu Ile Ala Lys  
210 215 220  
Met Val Asn Pro Ala Pro Lys Asp Asn Glu Asn Asn Asn Glu Asn Asn  
225 230 235 240  
Asn Glu Asn Asn Thr Lys Glu Asn Thr Lys Ser Glu Ser  
245 250

<210> 131  
<211> 655  
<212> DNA  
<213> Helicobacter pylori

<220>

<221> CDS  
<222> (31)...(600)

<400> 131

gtgcattatt taagaatttt aatactgagt atg agt ttt tta aat att tta aat	54
Met Ser Phe Leu Asn Ile Leu Asn	
1 5	
gct gaa aat ttg agt tat atg tct tct tct tat caa ata ggc acg gtg	102
Ala Glu Asn Leu Ser Tyr Met Ser Ser Ser Tyr Gln Ile Gly Thr Val	
10 15 20	
ttt atg cgc cct tta aac acc aac aag ctt tta caa ggg gct tca atc	150
Phe Met Arg Pro Leu Asn Thr Asn Lys Leu Leu Gln Gly Ala Ser Ile	
25 30 35 40	
ctt caa ggc tat gaa gtg aat cct aaa aac gat tgg gct tat tct agg	198
Leu Gln Gly Tyr Glu Val Asn Pro Lys Asn Asp Trp Ala Tyr Ser Arg	
45 50 55	
tat tat ttc ttt ata gat tat ggc aat gtg ctt ttt aat aat gac tct	246
Tyr Tyr Phe Phe Ile Asp Tyr Gly Asn Val Leu Phe Asn Asn Asp Ser	
60 65 70	
act tta caa gcg aac atg ttc act tat ggg gtg gga ggg gat ttt atg	294
Thr Leu Gln Ala Asn Met Phe Thr Tyr Gly Val Gly Gly Asp Phe Met	
75 80 85	
gtc gcc tac gct aaa aac cct atc aac cgc tgg gct ttt ttc ttt ggc	342
Val Ala Tyr Ala Lys Asn Pro Ile Asn Arg Trp Ala Phe Phe Phe Gly	
90 95 100	
ttg caa ctg gcc gct aac aca tgg ata ctc aac aat aaa gtc aaa gat	390
Leu Gln Leu Ala Ala Asn Thr Trp Ile Leu Asn Asn Lys Val Lys Asp	
105 110 115 120	
ttg gtg gtg aat act tgg gat tca tta aaa gat ttc aat ttt cac aac	438
Leu Val Val Asn Thr Trp Asp Ser Leu Lys Asp Phe Asn Phe His Asn	
125 130 135	
act tat ttc agg gct att ggg aag ttt ggg gtg cag ttt cgc acg atc	486
Thr Tyr Phe Arg Ala Ile Gly Lys Phe Gly Val Gln Phe Arg Thr Ile	
140 145 150	
gtt ttg tat cat aag gtg gat gta gaa att ggc atg aaa atc ttt cta	534
Val Leu Tyr His Lys Val Asp Val Glu Ile Gly Met Lys Ile Phe Leu	
155 160 165	
act cct gaa agg cgc agt ttg ttt gaa agg agc ttt ttg ttt ttt gtt	582
Thr Pro Glu Arg Arg Ser Leu Phe Glu Arg Ser Phe Leu Phe Phe Val	
170 175 180	
tcg cat tcg tgg cat ttt taaatggcgg agagagaggg attcgaaccc	630
Ser His Ser Trp His Phe	
185 190	
tcgaaggctt gcaccttaca cgcgt	655

<210> 132

<211> 190  
 <212> PRT  
 <213> Helicobacter pylori

<400> 132  
 Met Ser Phe Leu Asn Ile Leu Asn Ala Glu Asn Leu Ser Tyr Met Ser  
 1 5 10 15  
 Ser Ser Tyr Gln Ile Gly Thr Val Phe Met Arg Pro Leu Asn Thr Asn  
 20 25 30  
 Lys Leu Leu Gln Gly Ala Ser Ile Leu Gln Gly Tyr Glu Val Asn Pro  
 35 40 45  
 Lys Asn Asp Trp Ala Tyr Ser Arg Tyr Tyr Phe Phe Ile Asp Tyr Gly  
 50 55 60  
 Asn Val Leu Phe Asn Asn Asp Ser Thr Leu Gln Ala Asn Met Phe Thr  
 65 70 75 80  
 Tyr Gly Val Gly Gly Asp Phe Met Val Ala Tyr Ala Lys Asn Pro Ile  
 85 90 95  
 Asn Arg Trp Ala Phe Phe Phe Gly Leu Gln Leu Ala Ala Asn Thr Trp  
 100 105 110  
 Ile Leu Asn Asn Lys Val Lys Asp Leu Val Val Asn Thr Trp Asp Ser  
 115 120 125  
 Leu Lys Asp Phe Asn Phe His Asn Thr Tyr Phe Arg Ala Ile Gly Lys  
 130 135 140  
 Phe Gly Val Gln Phe Arg Thr Ile Val Leu Tyr His Lys Val Asp Val  
 145 150 155 160  
 Glu Ile Gly Met Lys Ile Phe Leu Thr Pro Glu Arg Arg Ser Leu Phe  
 165 170 175  
 Glu Arg Ser Phe Leu Phe Phe Val Ser His Ser Trp His Phe  
 180 185 190

<210> 133  
 <211> 830  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (31)...(714)

<400> 133  
 aaagcactat attaagatta ggatcattta atg gca gat aaa gaa ata ctg att 54  
 Met Ala Asp Lys Glu Ile Leu Ile  
 1 5  
 ttt gta gaa ggt cca agc gat aag gtg ttt tta gaa gtt tat ctg tat 102  
 Phe Val Glu Gly Pro Ser Asp Lys Val Phe Leu Glu Val Tyr Leu Tyr  
 10 15 20  
 ttt cta gaa aga ttt cca atc aaa aac ttt aaa gtg caa aat gta gat 150  
 Phe Leu Glu Arg Phe Pro Ile Lys Asn Phe Lys Val Gln Asn Val Asp  
 25 30 35 40  
 gga aaa gat aac ctg tct aaa cga ttg ctt gaa att gaa aaa tac gat 198  
 Gly Lys Asp Asn Leu Ser Lys Arg Leu Leu Glu Ile Glu Lys Tyr Asp  
 45 50 55  
 aaa aca ctt atc att ttt gat gcg gat aaa gac tat gag agt aat aaa 246  
 Lys Thr Leu Ile Ile Phe Asp Ala Asp Lys Asp Tyr Glu Ser Asn Lys  
 60 65 70



[illegible]

<400> 134

Met	Ala	Asp	Lys	Glu	Ile	Leu	Ile	Phe	Val	Glu	Gly	Pro	Ser	Asp	Lys
1				5					10					15	
Val	Phe	Leu	Glu	Val	Tyr	Leu	Tyr	Phe	Leu	Glu	Arg	Phe	Pro	Ile	Lys
			20					25					30		
Asn	Phe	Lys	Val	Gln	Asn	Val	Asp	Gly	Lys	Asp	Asn	Leu	Ser	Lys	Arg
		35					40					45			
Leu	Leu	Glu	Ile	Glu	Lys	Tyr	Asp	Lys	Thr	Leu	Ile	Phe	Asp	Ala	
	50					55					60				
Asp	Lys	Asp	Tyr	Glu	Ser	Asn	Lys	Lys	Glu	Ile	Leu	Lys	Ile	Val	Ser

65					70					75					80
Glu	Ser	Lys	Gln	Thr	Ile	Ser	Glu	Glu	Gln	Ile	Phe	Leu	Phe	Pro	Asn
				85					90					95	
Asn	Gln	Asp	Asp	Gly	Asp	Leu	Glu	Thr	Leu	Leu	Leu	Lys	Ile	Ala	Asn
			100					105					110		
His	Lys	Glu	Phe	Ile	Asn	Cys	Phe	Glu	Ser	Tyr	Leu	Asp	Cys	Ile	Lys
		115					120					125			
Lys	Lys	Glu	His	Tyr	Lys	Pro	Ile	Lys	Asn	Ile	Arg	Lys	Ser	Lys	Trp
		130				135					140				
Tyr	Ala	Tyr	Leu	Glu	Ala	Leu	Gly	Leu	Glu	Lys	Phe	Phe	Gln	Tyr	Thr
145					150					155					160
Trp	Asp	Thr	Lys	Lys	Lys	Asn	Asn	Lys	Lys	Lys	Leu	Ile	Ile	Asp	Asp
				165					170					175	
Lys	Asp	Gly	Asp	Glu	Ile	Glu	Ile	Lys	Asp	Gln	Tyr	Lys	Gly	Asp	Tyr
			180					185					190		
Glu	Glu	Leu	Lys	Lys	Val	Leu	Asp	Leu	Asn	Ser	Lys	Ser	Leu	Ile	Pro
		195					200					205			
Leu	Lys	Asn	Phe	Leu	Gly	Gln	Phe	Ala	Glu	Asn	Asn	Gln	Lys	Thr	Asn
		210				215					220				
Pro	Lys	Ile	Phe												
225															

<210> 135  
 <211> 1349  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (78)...(1298)

<400> 135	
aagaacaaat tgagcctgct accgctctca ctcaatggcc gcaaaaaacaa gaaaagaaaa	60
aatcataagg aaaaaat atg gca aaa agt att gaa ttg caa gag ata gaa	110
Met Ala Lys Ser Ile Glu Leu Gln Glu Ile Glu	
1 5 10	
gtg tgg gat ggc aat acc gct agt tct aac gct tta aga cag gct caa	158
Val Trp Asp Gly Asn Thr Ala Ser Ser Asn Ala Leu Arg Gln Ala Gln	
15 20 25	
att gat gtc atc gca gcc tat cct atc acc cca tca acg ccc att gtg	206
Ile Asp Val Ile Ala Ala Tyr Pro Ile Thr Pro Ser Thr Pro Ile Val	
30 35 40	
caa aat tat ggc tcg ttt aag gat aat ggc tat gtt gat ggc gaa ttc	254
Gln Asn Tyr Gly Ser Phe Lys Asp Asn Gly Tyr Val Asp Gly Glu Phe	
45 50 55	
gtt tta gtg gaa tct gag cat gcc gcc atg agc gca tgc gtg gga gct	302
Val Leu Val Glu Ser Glu His Ala Ala Met Ser Ala Cys Val Gly Ala	
60 65 70 75	
gcc gca gct gga ggg aga gtc agc act gcg act agc tct caa ggt ttg	350
Ala Ala Ala Gly Gly Arg Val Ser Thr Ala Thr Ser Ser Gln Gly Leu	
80 85 90	
gcg tta atg gta gag gtt tta tac cag gct tct gga atg cgt ttg cct	398
Ala Leu Met Val Glu Val Leu Tyr Gln Ala Ser Gly Met Arg Leu Pro	

95	100	105	
atc gtt ttg aat tta gtc aat cgt gct tta gca gcc cct ttg aat atc Ile Val Leu Asn Leu Val Asn Arg Ala Leu Ala Ala Pro Leu Asn Ile 110 115 120			446
cat ggc gat cat tct gat atg tat tta agc agg gat tct ggt tgg ata His Gly Asp His Ser Asp Met Tyr Leu Ser Arg Asp Ser Gly Trp Ile 125 130 135			494
agt tta tgc aca tgc aac ccc caa gaa gct tat gat ttc act tta atg Ser Leu Cys Thr Cys Asn Pro Gln Glu Ala Tyr Asp Phe Thr Leu Met 140 145 150 155			542
gcg ttt aga atc gca gag cat caa aag gtg cgc gtg cct act att gtc Ala Phe Arg Ile Ala Glu His Gln Lys Val Arg Val Pro Thr Ile Val 160 165 170			590
aat caa gac ggg ttt tta tgc tcg cac acc gtg caa aat gtc cgc cct Asn Gln Asp Gly Phe Leu Cys Ser His Thr Val Gln Asn Val Arg Pro 175 180 185			638
ttg agc gat gca gtg gct tac caa ttc gtg ggc gaa tac caa acc aag Leu Ser Asp Ala Val Ala Tyr Gln Phe Val Gly Glu Tyr Gln Thr Lys 190 195 200			686
cat tcc ctt ttg gat ttt gat aaa ccg gta agc tat ggc gcg caa gct His Ser Leu Leu Asp Phe Asp Lys Pro Val Ser Tyr Gly Ala Gln Ala 205 210 215			734
gaa gaa gaa tgg cat tat gag cat aaa gcc caa ctc cac cat gcc atc Glu Glu Glu Trp His Tyr Glu His Lys Ala Gln Leu His His Ala Ile 220 225 230 235			782
atg agc gcg tct tct gtg att gaa gaa gtg ttc aat gat ttc gct aaa Met Ser Ala Ser Ser Val Ile Glu Glu Val Phe Asn Asp Phe Ala Lys 240 245 250			830
ctc aca ggc agg caa tac cat tta acc aaa act ttc cag cta gaa gac Leu Thr Gly Arg Gln Tyr His Leu Thr Lys Thr Phe Gln Leu Glu Asp 255 260 265			878
gct gaa atc gct atc ttt gcg tta ggc act act tat gaa tca gcg atc Ala Glu Ile Ala Ile Phe Ala Leu Gly Thr Thr Tyr Glu Ser Ala Ile 270 275 280			926
gta gcg gct aaa gaa atg cgt aaa aaa ggc att aag gcc ggc gtg gct Val Ala Ala Lys Glu Met Arg Lys Lys Gly Ile Lys Ala Gly Val Ala 285 290 295			974
acc atc cat tcc ttg cgc ccc ttc cct tat gaa aga tta ggg cag gat Thr Ile His Ser Leu Arg Pro Phe Pro Tyr Glu Arg Leu Gly Gln Asp 300 305 310 315			1022
ttg aaa aat ctt aaa gct tta gcg att tta gac aag agc tct cca gcg Leu Lys Asn Leu Lys Ala Leu Ala Ile Leu Asp Lys Ser Ser Pro Ala 320 325 330			1070
ggc act atg ggg gcg atg ttt aat gaa gta acg agc gcg gtg tat caa			1118

Gly Thr Met Gly Ala Met Phe Asn Glu Val Thr Ser Ala Val Tyr Gln	
335 340 345	
acg caa ggg act aaa cac ccc gtg gtg tct aac tac att tat ggt tta	1166
Thr Gln Gly Thr Lys His Pro Val Val Ser Asn Tyr Ile Tyr Gly Leu	
350 355 360	
ggc gaa agg gat atg acg atc gcg cat tta tgc gaa att ttt gaa gaa	1214
Gly Glu Arg Asp Met Thr Ile Ala His Leu Cys Glu Ile Phe Glu Glu	
365 370 375	
atc aat gaa gac gct ctt aaa ggc acg ctc acg cac cct acc caa caa	1262
Ile Asn Glu Asp Ala Leu Lys Gly Thr Leu Thr His Pro Thr Gln Gln	
380 385 390 395	
ttc gta ggc ttg cac ggc cct aaa atg agc ttt ttt taaaaaggaa	1308
Phe Val Gly Leu His Gly Pro Lys Met Ser Phe Phe	
400 405	
atatcatgggt aaaagaagtc aaaacactca aagggttttag c	1349

<210> 136  
 <211> 407  
 <212> PRT  
 <213> Helicobacter pylori

Met Ala Lys Ser Ile Glu Leu Gln Glu Ile Glu Val Trp Asp Gly Asn	
1 5 10 15	
Thr Ala Ser Ser Asn Ala Leu Arg Gln Ala Gln Ile Asp Val Ile Ala	
20 25 30	
Ala Tyr Pro Ile Thr Pro Ser Thr Pro Ile Val Gln Asn Tyr Gly Ser	
35 40 45	
Phe Lys Asp Asn Gly Tyr Val Asp Gly Glu Phe Val Leu Val Glu Ser	
50 55 60	
Glu His Ala Ala Met Ser Ala Cys Val Gly Ala Ala Ala Gly Gly	
65 70 75 80	
Arg Val Ser Thr Ala Thr Ser Ser Gln Gly Leu Ala Leu Met Val Glu	
85 90 95	
Val Leu Tyr Gln Ala Ser Gly Met Arg Leu Pro Ile Val Leu Asn Leu	
100 105 110	
Val Asn Arg Ala Leu Ala Ala Pro Leu Asn Ile His Gly Asp His Ser	
115 120 125	
Asp Met Tyr Leu Ser Arg Asp Ser Gly Trp Ile Ser Leu Cys Thr Cys	
130 135 140	
Asn Pro Gln Glu Ala Tyr Asp Phe Thr Leu Met Ala Phe Arg Ile Ala	
145 150 155 160	
Glu His Gln Lys Val Arg Val Pro Thr Ile Val Asn Gln Asp Gly Phe	
165 170 175	
Leu Cys Ser His Thr Val Gln Asn Val Arg Pro Leu Ser Asp Ala Val	
180 185 190	
Ala Tyr Gln Phe Val Gly Glu Tyr Gln Thr Lys His Ser Leu Leu Asp	
195 200 205	
Phe Asp Lys Pro Val Ser Tyr Gly Ala Gln Ala Glu Glu Glu Trp His	
210 215 220	
Tyr Glu His Lys Ala Gln Leu His His Ala Ile Met Ser Ala Ser Ser	
225 230 235 240	
Val Ile Glu Glu Val Phe Asn Asp Phe Ala Lys Leu Thr Gly Arg Gln	
245 250 255	

Tyr His Leu Thr Lys Thr Phe Gln Leu Glu Asp Ala Glu Ile Ala Ile  
 260 265 270  
 Phe Ala Leu Gly Thr Thr Tyr Glu Ser Ala Ile Val Ala Ala Lys Glu  
 275 280 285  
 Met Arg Lys Lys Gly Ile Lys Ala Gly Val Ala Thr Ile His Ser Leu  
 290 295 300  
 Arg Pro Phe Pro Tyr Glu Arg Leu Gly Gln Asp Leu Lys Asn Leu Lys  
 305 310 315 320  
 Ala Leu Ala Ile Leu Asp Lys Ser Ser Pro Ala Gly Thr Met Gly Ala  
 325 330 335  
 Met Phe Asn Glu Val Thr Ser Ala Val Tyr Gln Thr Gln Gly Thr Lys  
 340 345 350  
 His Pro Val Val Ser Asn Tyr Ile Tyr Gly Leu Gly Glu Arg Asp Met  
 355 360 365  
 Thr Ile Ala His Leu Cys Glu Ile Phe Glu Glu Ile Asn Glu Asp Ala  
 370 375 380  
 Leu Lys Gly Thr Leu Thr His Pro Thr Gln Gln Phe Val Gly Leu His  
 385 390 395 400  
 Gly Pro Lys Met Ser Phe Phe  
 405

<210> 137  
 <211> 948  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (1)...(855)

<400> 137  
 aaa att gaa gtt tta agg ggt ttt ttg aaa cga gcg tta tac tta att 48  
 Lys Ile Glu Val Leu Arg Gly Phe Leu Lys Arg Ala Leu Tyr Leu Ile  
 1 5 10 15  
 tta ggg ctt ttt tac acg ctt aat gca gag agc ttt aaa gat gtt ttg 96  
 Leu Gly Leu Phe Tyr Thr Leu Asn Ala Glu Ser Phe Lys Asp Val Leu  
 20 25 30  
 act aaa gtg gat tac act ttt ttt aat aaa aag gtg gtt tcg ccc atc 144  
 Thr Lys Val Asp Tyr Thr Phe Phe Asn Lys Lys Val Val Ser Pro Ile  
 35 40 45  
 aaa cgc tat gcg gat aga tcg gcg ttt tat ctg ggg ctt ggg tat caa 192  
 Lys Arg Tyr Ala Asp Arg Ser Ala Phe Tyr Leu Gly Leu Gly Tyr Gln  
 50 55 60  
 tta ggg agc att cag cac aac tct agc aac ttg aat tta tcc cag caa 240  
 Leu Gly Ser Ile Gln His Asn Ser Ser Asn Leu Asn Leu Ser Gln Gln  
 65 70 75 80  
 ttc aat aag agt cag att att ttc agc gat agt cta agc cct gtt ttt 288  
 Phe Asn Lys Ser Gln Ile Ile Phe Ser Asp Ser Leu Ser Pro Val Phe  
 85 90 95  
 aaa aat tcg tat gtg tct aat ggc ctt ggc gtg caa gtg ggc tat aag 336  
 Lys Asn Ser Tyr Val Ser Asn Gly Leu Gly Val Gln Val Gly Tyr Lys  
 100 105 110

tgg gtg ggt aag cat gaa gag acg aaa tgg ttt ggc ttc agg tgg ggg Trp Val Gly Lys His Glu Glu Thr Lys Trp Phe Gly Phe Arg Trp Gly 115 120 125	384
ctg ttt tat gat ttg agc gcc tct ctt tat ggc caa aaa gaa tca cag Leu Phe Tyr Asp Leu Ser Ala Ser Leu Tyr Gly Gln Lys Glu Ser Gln 130 135 140	432
tct gtc atc att tcc act tac ggc act tat atg gat tta tta ttg aac Ser Val Ile Ile Ser Thr Tyr Gly Thr Tyr Met Asp Leu Leu Leu Asn 145 150 155 160	480
gct tat aat ggg gat aag ttt ttt gct ggg ttc aat ctg ggg att gct Ala Tyr Asn Gly Asp Lys Phe Phe Ala Gly Phe Asn Leu Gly Ile Ala 165 170 175	528
ttt gct gga gtg tat gac aaa gtg agc gat gcg tta ttg tat caa gcc Phe Ala Gly Val Tyr Asp Lys Val Ser Asp Ala Leu Leu Tyr Gln Ala 180 185 190	576
ctt ctt tta gac act ttt ggc ggg aaa gtg gat cca aat ggc ttc cag Leu Leu Leu Asp Thr Phe Gly Gly Lys Val Asp Pro Asn Gly Phe Gln 195 200 205	624
ttt ttg gta aat tta ggg gtt cgt tta ggg aat aag cac aac caa ttt Phe Leu Val Asn Leu Gly Val Arg Leu Gly Asn Lys His Asn Gln Phe 210 215 220	672
ggc ttt ggg att aaa atc cct act tat tat ttt aac cat tat tat tcc Gly Phe Gly Ile Lys Ile Pro Thr Tyr Tyr Phe Asn His Tyr Tyr Ser 225 230 235 240	720
atg aat aac att agc aat aat agt gaa gat gtc ctc aaa gtt tta cga Met Asn Asn Ile Ser Asn Asn Ser Glu Asp Val Leu Lys Val Leu Arg 245 250 255	768
ttt tta gaa tac ggg atc aac agc ttg tta tac caa gtt gat ttc agg Phe Leu Glu Tyr Gly Ile Asn Ser Leu Leu Tyr Gln Val Asp Phe Arg 260 265 270	816
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 20 25 30  
 Thr Lys Val Asp Tyr Thr Phe Phe Asn Lys Lys Val Val Ser Pro Ile  
 35 40 45

Lys Arg Tyr Ala Asp Arg Ser Ala Phe Tyr Leu Gly Leu Gly Tyr Gln  
 50 55 60  
 Leu Gly Ser Ile Gln His Asn Ser Ser Asn Leu Asn Leu Ser Gln Gln  
 65 70 75 80  
 Phe Asn Lys Ser Gln Ile Ile Phe Ser Asp Ser Leu Ser Pro Val Phe  
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 Lys Asn Ser Tyr Val Ser Asn Gly Leu Gly Val Gln Val Gly Tyr Lys  
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 115 120 125  
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 130 135 140  
 Ser Val Ile Ile Ser Thr Tyr Gly Thr Tyr Met Asp Leu Leu Leu Asn  
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 Ala Tyr Asn Gly Asp Lys Phe Phe Ala Gly Phe Asn Leu Gly Ile Ala  
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 Phe Ala Gly Val Tyr Asp Lys Val Ser Asp Ala Leu Leu Tyr Gln Ala  
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 Phe Leu Val Asn Leu Gly Val Arg Leu Gly Asn Lys His Asn Gln Phe  
 210 215 220  
 Gly Phe Gly Ile Lys Ile Pro Thr Tyr Tyr Phe Asn His Tyr Tyr Ser  
 225 230 235 240  
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 245 250 255  
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 Thr Ile Gly Leu Gly Val Ile Ala Leu Phe Leu Gly Leu Leu Asn Pro  
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 ttg agt gcg gcg agt tac ccc ccc att aaa aac act aaa gta ggc tta 151  
 Leu Ser Ala Ala Ser Tyr Pro Pro Ile Lys Asn Thr Lys Val Gly Leu  
 25 30 35  
 gcc ctt tct agc cac ccg cta gct agt gag atc ggg caa aag gtt tta 199  
 Ala Leu Ser Ser His Pro Leu Ala Ser Glu Ile Gly Gln Lys Val Leu  
 40 45 50 55  
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 Glu Glu Gly Gly Asn Ala Ile Asp Ala Ala Val Ala Ile Gly Phe Ala

				60				65				70				
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Leu	Ala	Val	Val	His	Pro	Ala	Ala	Gly	Asn	Ile	Gly	Gly	Gly	Gly	Phe	
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gcg	gtt	atc	cat	ttg	gct	aat	ggg	gaa	aat	gtt	gcg	tta	gat	ttt	aga	343
Ala	Val	Ile	His	Leu	Ala	Asn	Gly	Glu	Asn	Val	Ala	Leu	Asp	Phe	Arg	
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gaa	aaa	gcc	ccc	tta	aaa	gcc	act	aaa	aac	atg	ttt	tta	gac	aag	caa	391
Glu	Lys	Ala	Pro	Leu	Lys	Ala	Thr	Lys	Asn	Met	Phe	Leu	Asp	Lys	Gln	
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ggc	aat	gta	gtc	cct	aaa	ctc	agc	gaa	gat	ggc	tat	ttg	gcg	gcc	ggg	439
Gly	Asn	Val	Val	Pro	Lys	Leu	Ser	Glu	Asp	Gly	Tyr	Leu	Ala	Ala	Gly	
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Val	Pro	Gly	Thr	Val	Ala	Gly	Met	Glu	Ala	Met	Leu	Lys	Lys	Tyr	Gly	
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act	aaa	aaa	cta	tcg	caa	ctc	att	gat	cct	gcc	att	aaa	ttg	gct	gaa	535
Thr	Lys	Lys	Leu	Ser	Gln	Leu	Ile	Asp	Pro	Ala	Ile	Lys	Leu	Ala	Glu	
				155				160				165				
aat	ggg	tat	gcg	att	tca	caa	aga	caa	gca	gaa	acc	cta	aag	gaa	gca	583
Asn	Gly	Tyr	Ala	Ile	Ser	Gln	Arg	Gln	Ala	Glu	Thr	Leu	Lys	Glu	Ala	
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Arg	Glu	Arg	Phe	Leu	Lys	Tyr	Ser	Ser	Ser	Lys	Lys	Tyr	Phe	Phe	Lys	
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Lys	Gly	His	Leu	Asp	Tyr	Gln	Glu	Gly	Asp	Leu	Phe	Val	Gln	Lys	Asp	
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Leu	Ala	Lys	Thr	Leu	Asn	Gln	Ile	Lys	Thr	Leu	Gly	Ala	Lys	Gly	Phe	
				220				225				230				
tat	caa	ggg	caa	gtc	gct	gag	ctt	att	gag	aaa	gac	atg	aaa	aaa	aat	775
Tyr	Gln	Gly	Gln	Val	Ala	Glu	Leu	Ile	Glu	Lys	Asp	Met	Lys	Lys	Asn	
				235				240				245				
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Gly	Gly	Ile	Ile	Thr	Lys	Glu	Asp	Leu	Ala	Ser	Tyr	Asn	Val	Lys	Trp	
250								255				260				
cgc	aaa	ccc	gtg	gta	ggg	agt	tat	cgt	ggg	tat	aag	atc	att	tct	atg	871
Arg	Lys	Pro	Val	Val	Gly	Ser	Tyr	Arg	Gly	Tyr	Lys	Ile	Ile	Ser	Met	
265								270				275				
tcg	ccg	cca	agt	tcg	gga	ggc	acg	cat	ttg	atc	cag	att	tta	aat	gtc	919
Ser	Pro	Pro	Ser	Ser	Gly	Gly	Thr	His	Leu	Ile	Gln	Ile	Leu	Asn	Val	
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atc	cat	atc	gct	gcc	gaa	gcg	atg	cgt	cag	gct	tat	gcg	gat	aga	tcg		1015
Ile	His	Ile	Ala	Ala	Glu	Ala	Met	Arg	Gln	Ala	Tyr	Ala	Asp	Arg	Ser		
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Val	Tyr	Met	Gly	Asp	Ala	Asp	Phe	Val	Ser	Val	Pro	Val	Asp	Lys	Leu		
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Ile	Asn	Lys	Ala	Tyr	Ala	Lys	Lys	Ile	Phe	Asp	Thr	Ile	Gln	Pro	Asp		
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Thr	Val	Thr	Pro	Ser	Ser	Gln	Ile	Lys	Pro	Gly	Met	Gly	Gln	Leu	His		
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gag	ggg	agc	aat	acc	acg	cat	tat	tct	gta	gcg	gac	agg	tgg	ggg	aat		1207
Glu	Gly	Ser	Asn	Thr	Thr	His	Tyr	Ser	Val	Ala	Asp	Arg	Trp	Gly	Asn		
			380						385					390			
gca	gtc	agc	gtt	act	tac	acc	att	aac	gct	tct	tat	gga	agc	gct	gcc		1255
Ala	Val	Ser	Val	Thr	Tyr	Thr	Ile	Asn	Ala	Ser	Tyr	Gly	Ser	Ala	Ala		
			395					400					405				
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Ser	Ile	Asp	Gly	Ala	Gly	Phe	Leu	Leu	Asn	Asn	Glu	Met	Asp	Asp	Phe		
		410				415						420					
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Ser	Ile	Lys	Pro	Gly	Asn	Pro	Asn	Leu	Tyr	Gly	Leu	Val	Gly	Gly	Asp		
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gcg	aat	gcg	att	gaa	gcc	aat	aag	cgc	cct	tta	agc	tcc	atg	tcg	cct		1399
Ala	Asn	Ala	Ile	Glu	Ala	Asn	Lys	Arg	Pro	Leu	Ser	Ser	Met	Ser	Pro		
	440				445				450						455		
acg	att	gtg	ttg	aaa	aac	aat	aag	gtt	ttt	ttg	gtg	gtg	gga	agc	cct		1447
Thr	Ile	Val	Leu	Lys	Asn	Asn	Lys	Val	Phe	Leu	Val	Val	Gly	Ser	Pro		
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gga	ggg	tct	agg	att	atc	act	acg	gtg	ctg	caa	gtg	att	tct	aat	gtc		1495
Gly	Gly	Ser	Arg	Ile	Ile	Thr	Thr	Val	Leu	Gln	Val	Ile	Ser	Asn	Val		
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Ile	Asp	Tyr	Asn	Met	Asn	Ile	Ser	Glu	Ala	Val	Ser	Ala	Pro	Arg	Phe		
		490					495					500					
cac	atg	caa	tgg	ctc	cct	gat	gaa	tta	agg	att	gaa	aag	ttt	ggc	atg		1591
His	Met	Gln	Trp	Leu	Pro	Asp	Glu	Leu	Arg	Ile	Glu	Lys	Phe	Gly	Met		
	505					510					515						
ccc	gct	gat	gtg	aaa	gac	aac	ctc	act	aaa	atg	ggc	tat	caa	atc	gtt		1639
Pro	Ala	Asp	Val	Lys	Asp	Asn	Leu	Thr	Lys	Met	Gly	Tyr	Gln	Ile	Val		
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act aag ccg gtc atg ggt gat gtg aat gcg atc caa gtt ttg cct aaa 1687  
 Thr Lys Pro Val Met Gly Asp Val Asn Ala Ile Gln Val Leu Pro Lys  
 540 545 550

act aaa ggg agc gtt ttc tat ggt tca acg gat cca agg aaa gaa ttt 1735  
 Thr Lys Gly Ser Val Phe Tyr Gly Ser Thr Asp Pro Arg Lys Glu Phe  
 555 560 565

taattcttttg tcatatacag gtttttaatc ctatttagcc ttatttttttg ggatggaggg 1795  
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 Lys Asn Thr Lys Val Gly Leu Ala Leu Ser Ser His Pro Leu Ala Ser  
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 Glu Ile Gly Gln Lys Val Leu Glu Glu Gly Gly Asn Ala Ile Asp Ala  
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 Ala Val Ala Ile Gly Phe Ala Leu Ala Val Val His Pro Ala Ala Gly  
 65 70 75 80  
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 85 90 95  
 Asn Val Ala Leu Asp Phe Arg Glu Lys Ala Pro Leu Lys Ala Thr Lys  
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 Pro Ala Ile Lys Leu Ala Glu Asn Gly Tyr Ala Ile Ser Gln Arg Gln  
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 Ala Glu Thr Leu Lys Glu Ala Arg Glu Arg Phe Leu Lys Tyr Ser Ser  
 180 185 190  
 Ser Lys Lys Tyr Phe Phe Lys Lys Gly His Leu Asp Tyr Gln Glu Gly  
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 Asp Leu Phe Val Gln Lys Asp Leu Ala Lys Thr Leu Asn Gln Ile Lys  
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 Thr Leu Gly Ala Lys Gly Phe Tyr Gln Gly Gln Val Ala Glu Leu Ile  
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 Ala Ser Tyr Asn Val Lys Trp Arg Lys Pro Val Val Gly Ser Tyr Arg  
 260 265 270  
 Gly Tyr Lys Ile Ile Ser Met Ser Pro Pro Ser Ser Gly Gly Thr His  
 275 280 285  
 Leu Ile Gln Ile Leu Asn Val Met Glu Asn Ala Asp Leu Ser Ala Leu  
 290 295 300  
 Gly Tyr Gly Ala Ser Lys Asn Ile His Ile Ala Ala Glu Ala Met Arg  
 305 310 315 320  
 Gln Ala Tyr Ala Asp Arg Ser Val Tyr Met Gly Asp Ala Asp Phe Val  
 325 330 335

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Ser Val Pro Val Asp Lys Leu Ile Asn Lys Ala Tyr Ala Lys Lys Ile  
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 Phe Asp Thr Ile Gln Pro Asp Thr Val Thr Pro Ser Ser Gln Ile Lys  
 355 360 365  
 Pro Gly Met Gly Gln Leu His Glu Gly Ser Asn Thr Thr His Tyr Ser  
 370 375 380  
 Val Ala Asp Arg Trp Gly Asn Ala Val Ser Val Thr Tyr Thr Ile Asn  
 385 390 395 400  
 Ala Ser Tyr Gly Ser Ala Ala Ser Ile Asp Gly Ala Gly Phe Leu Leu  
 405 410 415  
 Asn Asn Glu Met Asp Asp Phe Ser Ile Lys Pro Gly Asn Pro Asn Leu  
 420 425 430  
 Tyr Gly Leu Val Gly Gly Asp Ala Asn Ala Ile Glu Ala Asn Lys Arg  
 435 440 445  
 Pro Leu Ser Ser Met Ser Pro Thr Ile Val Leu Lys Asn Asn Lys Val  
 450 455 460  
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 465 470 475 480  
 Leu Gln Val Ile Ser Asn Val Ile Asp Tyr Asn Met Asn Ile Ser Glu  
 485 490 495  
 Ala Val Ser Ala Pro Arg Phe His Met Gln Trp Leu Pro Asp Glu Leu  
 500 505 510  
 Arg Ile Glu Lys Phe Gly Met Pro Ala Asp Val Lys Asp Asn Leu Thr  
 515 520 525  
 Lys Met Gly Tyr Gln Ile Val Thr Lys Pro Val Met Gly Asp Val Asn  
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 Thr Asp Pro Arg Lys Glu Phe  
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 Met Gln Asn His Asp Leu Glu Ser Ile Lys Gln Ala  
 1 5 10  
 gct ttg att gaa tat gaa gtg aga gaa caa ggc tct agt att gtg cta 159  
 Ala Leu Ile Glu Tyr Glu Val Arg Glu Gln Gly Ser Ser Ile Val Leu  
 15 20 25  
 gac agc aat att tcc aaa gag cct tta gag ttt att ata ggc act aat 207  
 Asp Ser Asn Ile Ser Lys Glu Pro Leu Glu Phe Ile Ile Gly Thr Asn  
 30 35 40  
 caa atc ata gca ggg tta gaa aag gcg gta tta aag gct caa att ggc 255  
 Gln Ile Ile Ala Gly Leu Glu Lys Ala Val Leu Lys Ala Gln Ile Gly  
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<211> 185
<212> PRT
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Ser	Lys	Glu	Pro	Leu	Glu	Phe	Ile	Ile	Gly	Thr	Asn	Gln	Ile	Ile	Ala
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Val	Val	Ile	Ala	Pro	Glu	Glu	Ala	Tyr	Gly	Val	Tyr	Glu	Ser	Ser	Tyr
65					70					75					80
Leu	Gln	Glu	Val	Pro	Arg	Asp	Gln	Phe	Glu	Gly	Ile	Glu	Leu	Glu	Lys
				85					90					95	
Gly	Met	Ser	Val	Phe	Gly	Gln	Thr	Glu	Asp	Asn	Gln	Thr	Ile	Gln	Ala
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Ile	Ile	Lys	Asp	Phe	Ser	Ala	Thr	His	Val	Met	Val	Asp	Tyr	Asn	His
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Pro	Leu	Ala	Gly	Lys	Thr	Leu	Ala	Phe	Arg	Phe	Lys	Val	Leu	Gly	Phe
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<400> 143

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<400> 144

-161-

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Ser Ala Cys Phe	Ser Phe Cys Asn Cys Phe Ala Asn Ala Ser Asn Ser	100	110

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	Glu His Asn Thr Asn Ile Ala Thr Glu Phe Arg Ala Gly Leu Thr Thr	
	10 15 20	
	ttt atc acc atg att tac atc gtg ccc tta aac gct ctt atc ctt tct	150
	Phe Ile Thr Met Ile Tyr Ile Val Pro Leu Asn Ala Leu Ile Leu Ser	
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	caa gcc aac atg cct tat gaa gcc ctt tta agt gca acg gcc att atc	198
	Gln Ala Asn Met Pro Tyr Glu Ala Leu Leu Ser Ala Thr Ala Ile Ile	
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	act atc tta tcg agc gtg ttt aac gga ttg tgg gca aac acc cct atc	246
	Thr Ile Leu Ser Ser Val Phe Asn Gly Leu Trp Ala Asn Thr Pro Ile	
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	Ala Met Ser Val Gly Leu Gly Leu Ser Ala Tyr Phe Ser Phe Gly Leu	
	75 80 85	
	gtt caa ggg tta aaa ctc cct tgg cag agc gct tta ggc atc gta gcg	342
	Val Gln Gly Leu Lys Leu Pro Trp Gln Ser Ala Leu Gly Ile Val Ala	
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	ctc tcg gga gcg att ttt gtg att ttg tct ttc act aaa ttt aga agt	390
	Leu Ser Gly Ala Ile Phe Val Ile Leu Ser Phe Thr Lys Phe Arg Ser	
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	Trp Val Met Arg Ser Ile Pro Ser Asp Leu Arg Arg Ala Val Ser Ala	
	120 125 130 135	
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	Gly Ile Gly Ala Phe Ile Ala Phe Ile Gly Leu Lys Glu Met His Ile	
	140 145 150	
	gtc gtt acc cat aar gct acg ctt gta acc tta ggc gat ttt ggc gat	534

0085913-062901

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Pro	His	Val	Leu	Leu	Gly	Val	Val	Gly	Ile	Ile	Leu	Thr	Phe	Ala	Leu	
		170					175					180				
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Tyr	Thr	Leu	Lys	Ile	Arg	Gly	Ser	Phe	Ile	Ile	Ala	Val	Leu	Ile	Thr	
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Ser	Ile	Leu	Ala	Trp	Val	Leu	Lys	Leu	Ala	Pro	Tyr	Pro	Ser	Glu	Phe	
200				205						210					215	
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Phe	Ser	Met	Pro	Ala	Ser	Ile	Gly	Pro	Ile	Ala	Phe	Gln	Leu	Asp	Phe	
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Lys	Gly	Ile	Phe	Phe	Asp	Ala	Ser	Gly	Ala	Phe	Thr	Leu	Ala	Leu	Val	
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cca	gtt	att	atc	act	ttt	ttt	gta	acc	gat	ttg	ttt	gat	tct	tta	ggc	822
Pro	Val	Ile	Ile	Thr	Phe	Phe	Val	Thr	Asp	Leu	Phe	Asp	Ser	Leu	Gly	
		250					255					260				
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Thr	Leu	Ala	Gly	Ile	Gly	His	Lys	Thr	Asp	Phe	Phe	Asn	Asp	Glu	Glu	
	265					270					275					
aaa	aac	aag	gaa	ttg	gaa	aag	act	ttg	gaa	gcg	gat	gcg	gtg	gct	tct	918
Lys	Asn	Lys	Glu	Leu	Glu	Lys	Thr	Leu	Glu	Ala	Asp	Ala	Val	Ala	Ser	
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Leu	Gly	Ser	Ala	Val	Val	Gly	Val	Ser	Thr	Thr	Thr	Ala	Phe	Ile	Glu	
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agc	gcg	agt	ggg	gtt	gaa	gag	ggg	ggc	cgc	aca	ggg	ctt	aca	gcg	gtt	1014
Ser	Ala	Ser	Gly	Val	Glu	Glu	Gly	Gly	Arg	Thr	Gly	Leu	Thr	Ala	Val	
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Phe	Thr	Gly	Leu	Phe	Phe	Val	Leu	Thr	Leu	Phe	Cys	Leu	Pro	Leu	Leu	
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Lys	Ala	Ile	Pro	Ser	Asn	Ala	Ile	Tyr	Pro	Val	Leu	Val	Val	Val	Gly	
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gtt	ttg	atg	ttt	agc	gtg	tta	gag	ggg	gtg	aat	ttt	aaa	gac	atg	gcc	1158
Val	Leu	Met	Phe	Ser	Val	Leu	Glu									







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acg	cct	gat	ttt	gaa	ttg	agt	tta	aga	gcg	tat	caa	aca	gca	aag	cgt		494
Thr	Pro	Asp	Phe	Glu	Leu	Ser	Leu	Arg	Ala	Tyr	Gln	Thr	Ala	Lys	Arg		
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Leu	Gly	Ile	Asp	Leu	Lys	Val	Gly	Asn	Val	Phe	Ser	Ser	Asp	Phe	Phe		
	145					150					155						
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Tyr	Ser	Phe	Glu	Thr	His	Ala	Phe	Asp	Leu	Met	Ala	Lys	Tyr	Asn	His		
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Leu	Ala	Ile	Glu	Met	Glu	Ala	Ala	Gly	Leu	Tyr	Ala	Thr	Ala	Met	Glu		
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Leu	Asn	Ala	Lys	Ala	Leu	Cys	Leu	Cys	Ser	Val	Ser	Asp	His	Leu	Ile		
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Thr	Lys	Glu	Ala	Leu	Ser	Pro	Lys	Glu	Arg	Val	Glu	Ser	Phe	Asp	Asn		
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Leu	Gln	Asp	Ala	Lys	Glu	Ile	Thr	Asn	Val	Arg	Asn	Met	Leu	Gly	Phe		
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Ser	Gly	Lys	Tyr	Lys	Gly	Arg	Gly	Ile	Ser	Leu	Met	Gly	His	Gly	Met		
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Gly	Ile	Ala	Ser	Cys	Thr	Ile	Tyr	Val	Thr	Glu	Leu	Ile	Lys	Thr	Tyr		
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Gln	Val	Lys	Glu	Leu	Leu	Arg	Ile	Gly	Thr	Cys	Gly	Ala	Ile	Ser	Pro		
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Pro	Asp	Phe	Glu	Leu	Ser	Leu	Arg	Ala	Tyr	Gln	Thr	Ala	Lys	Arg	Leu		
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Ser Phe Glu Thr His Ala Phe Asp Leu Met Ala Lys Tyr Asn His Leu  
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Ala Ile Glu Met Glu Ala Ala Gly Leu Tyr Ala Thr Ala Met Glu Leu  
180 185 190  
Asn Ala Lys Ala Leu Cys Leu Cys Ser Val Ser Asp His Leu Ile Thr  
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Ser Ser Leu Arg Phe Leu Gly Leu Phe Ile Val Leu Pro Val Ile Ser  
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ttg tat gcg gat agt ttc cat tca agc agt ccc tta ctc gtg ggg ttg 207  
Leu Tyr Ala Asp Ser Phe His Ser Ser Ser Pro Leu Leu Val Gly Leu  
30 35 40  
gct gtg ggc gga gcg tat ctt acg caa att gtt ttt caa acc ccc atg 255  
Ala Val Gly Gly Ala Tyr Leu Thr Gln Ile Val Phe Gln Thr Pro Met  
45 50 55  
ggc att ctt agc gat aag ata ggc cgt aaa gtg gtg gtt atg gtg tgc 303  
Gly Ile Leu Ser Asp Lys Ile Gly Arg Lys Val Val Val Met Val Cys  
60 65 70 75  
ttg ctg ttg ttt tta gcc ggc tcg tta gtg tgc ttt ata gcg aat gat 351  
Leu Leu Leu Phe Leu Ala Gly Ser Leu Val Cys Phe Ile Ala Asn Asp  
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Ile Val Trp Leu Val Ile Gly Arg Phe Ile Gln Gly Met Gly Ala Leu  
95 100 105  
ggg ggg gtt att agt gcg atg gtg gcg gat gaa gtg aaa gaa gaa gag 447  
Gly Gly Val Ile Ser Ala Met Val Ala Asp Glu Val Lys Glu Glu Glu  
110 115 120  
cgc acc aaa gcc atg gcc atc atg gga gcg ttt att ttc att agc ttc 495  
Arg Thr Lys Ala Met Ala Ile Met Gly Ala Phe Ile Phe Ile Ser Phe  
125 130 135  
act ata agc atg gcg att ggc cct ggg gtt gta gcg ttt ttg ggg ggg 543

Thr	Ile	Ser	Met	Ala	Ile	Gly	Pro	Gly	Val	Val	Ala	Phe	Leu	Gly	Gly		
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Ala	Lys	Trp	Leu	Phe	Leu	Leu	Thr	Ala	Ile	Leu	Thr	Leu	Leu	Ser	Leu		
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Leu	Met	Leu	Leu	Lys	Val	Lys	Asp	Ala	Pro	Lys	Ile	Ser	Tyr	Gln	Ile		
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aaa	aac	ata	aaa	gct	tac	caa	ccc	aac	tct	aaa	gcc	ttg	tat	ctt	ttg	687	
Lys	Asn	Ile	Lys	Ala	Tyr	Gln	Pro	Asn	Ser	Lys	Ala	Leu	Tyr	Leu	Leu		
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Tyr	Leu	Ser	Ser	Phe	Phe	Glu	Lys	Ala	Phe	Met	Thr	Leu	Ile	Phe	Val		
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Leu	Ile	Pro	Leu	Ala	Leu	Val	Asn	Glu	Phe	His	Lys	Asp	Glu	Ser	Phe		
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Leu	Ile	Leu	Val	Tyr	Val	Pro	Gly	Ala	Leu	Leu	Gly	Val	Leu	Ser	Met		
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Gly	Ile	Ala	Ser	Val	Met	Ala	Glu	Lys	Tyr	Asn	Lys	Pro	Lys	Gly	Val		
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Gly	Val	Ala	Phe	Phe	Phe	Ile	Gly	Phe	Ala	Thr	Leu	Glu	Pro	Ile	Met		
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caa	tct	tta	gcg	tct	aaa	ttc	gcc	aaa	gtg	cat	gaa	aaa	ggc	aag	gtt	1071	
Gln	Ser	Leu	Ala	Ser	Lys	Phe	Ala	Lys	Val	His	Glu	Lys	Gly	Lys	Val		
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Leu	Gly	Gln	Phe	Thr	Thr	Phe	Gly	Tyr	Leu	Gly	Ser	Phe	Val	Gly	Gly		
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gtg	agc	ggg	ggg	ttg	agc	tac	cat	cat	tta	ggc	gtt	tct	aac	aca	agc	1167	
Val	Ser	Gly	Gly	Leu	Ser	Tyr	His	His	Leu	Gly	Val	Ser	Asn	Thr	Ser		
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Leu	Ile	Val	Val	Ala	Leu	Gly	Leu	Ile	Trp	Gly	Leu	Ser	Leu	Phe	Leu		
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ctc aac aac cct tcc aag caa aaa aat gtc tat ttc ccc tta gac gct 1263  
 Leu Asn Asn Pro Ser Lys Gln Lys Asn Val Tyr Phe Pro Leu Asp Ala  
 380 385 390 395

tac aat gag gaa caa ttt gaa act tta gag gat aaa atc att gaa tgg 1311  
 Tyr Asn Glu Glu Gln Phe Glu Thr Leu Glu Asp Lys Ile Ile Glu Trp  
 400 405 410

tat gtt aat att agc gaa gaa atc att att gtg aaa tat aat tcc gat 1359  
 Tyr Val Asn Ile Ser Glu Glu Ile Ile Ile Val Lys Tyr Asn Ser Asp  
 415 420 425

cac att agc gaa gaa gaa atc att cac tta gcg caa aac ttt aga aaa 1407  
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 35 40 45  
 Tyr Leu Thr Gln Ile Val Phe Gln Thr Pro Met Gly Ile Leu Ser Asp  
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 Lys Ile Gly Arg Lys Val Val Val Met Val Cys Leu Leu Leu Phe Leu  
 65 70 75 80  
 Ala Gly Ser Leu Val Cys Phe Ile Ala Asn Asp Ile Val Trp Leu Val  
 85 90 95  
 Ile Gly Arg Phe Ile Gln Gly Met Gly Ala Leu Gly Gly Val Ile Ser  
 100 105 110  
 Ala Met Val Ala Asp Glu Val Lys Glu Glu Glu Arg Thr Lys Ala Met  
 115 120 125  
 Ala Ile Met Gly Ala Phe Ile Phe Ile Ser Phe Thr Ile Ser Met Ala  
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 145 150 155 160  
 Leu Leu Thr Ala Ile Leu Thr Leu Leu Ser Leu Leu Met Leu Leu Lys  
 165 170 175  
 Val Lys Asp Ala Pro Lys Ile Ser Tyr Gln Ile Lys Asn Ile Lys Ala  
 180 185 190  
 Tyr Gln Pro Asn Ser Lys Ala Leu Tyr Leu Leu Tyr Leu Ser Ser Phe  
 195 200 205  
 Phe Glu Lys Ala Phe Met Thr Leu Ile Phe Val Leu Ile Pro Leu Ala  
 210 215 220  
 Leu Val Asn Glu Phe His Lys Asp Glu Ser Phe Leu Ile Leu Val Tyr  
 225 230 235 240  
 Val Pro Gly Ala Leu Leu Gly Val Leu Ser Met Gly Ile Ala Ser Val  
 245 250 255  
 Met Ala Glu Lys Tyr Asn Lys Pro Lys Gly Val Met Leu Ser Gly Val  
 260 265 270  
 Leu Leu Phe Ile Val Ser Tyr Leu Cys Leu Phe Leu Ala Asp Ser Ser



	90				95				100								
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ggc	atg	atc	atg	act	tta	gtc	aaa	gat	tat	cgt	aaa	gag	att	ttg	tgg	496	
Gly	Met	Ile	Met	Thr	Leu	Val	Lys	Asp	Tyr	Arg	Lys	Glu	Ile	Leu	Trp		
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ctt	gat	ttg	gtt	ttg	aaa	gtg	ggc	gtt	att	ggg	gaa	ttg	tta	agc	att	544	
Leu	Asp	Leu	Val	Leu	Lys	Val	Gly	Val	Ile	Gly	Glu	Leu	Leu	Ser	Ile		
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Phe	Gly	Leu	Val	Val	Val	Asp	Gly	Val	Tyr	Ser	His	Gly	Leu	Gly	Met		
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Asp	Leu	Ile	Lys	Asp	Leu	Gly	Ile	Leu	Ile	Val	Phe	Leu	Ile	Leu	Ile		
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Ile	Val	Ala	Phe	Gln	Ile	Phe	Lys	Thr	Leu	Phe	Trp	Trp	Phe	Pro	His		
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Arg	Phe	Ser	Leu	Met	Leu	Phe	Phe	Ser	Leu	Val	Ala	Ile	Val	Val	Trp		
			220					225					230				
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Leu	Lys	Ile	Glu	Met	Val	Leu	Gly	Ala	Phe	Leu	Ala	Gly	Leu	Val	Val		
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gtg	ggt	ttt	ggg	ttt	ttt	gtg	cct	ttg	ttt	ttc	atc	cat	gta	ggc	tct	928	
Val	Gly	Phe	Gly	Phe	Phe	Val	Pro	Leu	Phe	Phe	Ile	His	Val	Gly	Ser		
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Thr	Leu	Asp	Leu	Lys	Leu	Val	Phe	Leu	Asn	Pro	His	Leu	Ile	Leu	Gln		
				285					290					295			
ggg	ata	ttg	att	gtc	ata	gcg	atg	ttg	agt	ttg	cac	ttg	atc	act	tca	1024	
Gly	Ile	Leu	Ile	Val	Ile	Ala	Met	Leu	Ser	Leu	His	Leu	Ile	Thr	Ser		
			300					305					310				

Phe Ala Leu Gly Ala Ser Met Pro Leu Thr Phe Leu Val Thr Thr Ala  
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gca gta ggc tta aaa gcg caa gcg atc tca caa aac acc tac tac gca 1168  
 Ala Val Gly Leu Lys Ala Gln Ala Ile Ser Gln Asn Thr Tyr Tyr Ala  
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 365 370 375

aaa ata ctc aac aaa aaa gct tgaatgaaag cttaagcgctc taaatattta 1267  
 Lys Ile Leu Asn Lys Lys Ala

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Glu Ile Leu Phe Gly Ser Val Gly Ala Tyr Val Gly Phe Ile Glu Pro  
 35 40 45

Thr Lys Gly Phe Glu Ile Met Ser Glu Ile Gly Phe Leu Phe Leu Met  
 50 55 60

Phe Leu Cys Gly Leu Glu Val Glu Ile Tyr Leu Phe Lys Lys Leu Gly  
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Val Ser Leu Leu Lys Arg Ile Phe Ala Tyr Leu Leu Ile Leu Tyr Thr  
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Leu Ser Phe Ile Leu Thr Phe Ser Leu Asn Leu Glu Pro Ile Phe Met  
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Val Ile Phe Pro Ile Ile Ser Leu Gly Met Ile Met Thr Leu Val Lys  
 115 120 125

Asp Tyr Arg Lys Glu Ile Leu Trp Leu Asp Leu Val Leu Lys Val Gly  
 130 135 140

Val Ile Gly Glu Leu Leu Ser Ile Phe Gly Leu Val Val Val Asp Gly  
 145 150 155 160

Val Tyr Ser His Gly Leu Gly Met Asp Leu Ile Lys Asp Leu Gly Ile  
 165 170 175

Leu Ile Val Phe Leu Ile Leu Ile Ile Val Ala Phe Gln Ile Phe Lys  
 180 185 190

Thr Leu Phe Trp Trp Phe Pro His Leu Lys Leu Phe Val Met Pro Lys  
 195 200 205

Ser Ser Gln Phe Asn Gln Asp Val Arg Phe Ser Leu Met Leu Phe Phe  
 210 215 220

Ser Leu Val Ala Ile Val Val Trp Leu Lys Ile Glu Met Val Leu Gly  
 225 230 235 240

Ala Phe Leu Ala Gly Leu Val Val Ser Thr Phe Phe Pro His Lys Ser  
 245 250 255

Glu Leu Ile His Lys Leu Asn Asp Val Gly Phe Gly Phe Phe Val Pro  
 260 265 270

Leu Phe Phe Ile His Val Gly Ser Thr Leu Asp Leu Lys Leu Val Phe



275	280	285
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290	295	300
Leu Ser Leu His Leu Ile	Thr Ser Thr Leu Leu Trp	Arg Lys Tyr Phe
305	310	315
Lys Glu Ala Lys His Leu Phe	Ser Phe Ala Leu Gly	Ala Ser Met Pro
325	330	335
Leu Thr Phe Leu Val Thr Thr	Ala Ala Val Gly Leu Lys	Ala Gln Ala
340	345	350
Ile Ser Gln Asn Thr Tyr Tyr	Ala Leu Leu Met Ala Ala	Ile Phe Glu
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Lys Arg Val Arg Glu Leu Val Lys Lys His Pro Glu Lys Ser Ser Val	
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Ala Leu Val Val Leu Thr His Ala Ala Cys Lys Lys Ala Lys Glu Leu	
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Asp Asp Lys Val Gln Asp Lys Ser Lys Gln Ala Glu Lys Glu Asn Gln	
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Ile Asn Trp Trp Lys Tyr Ser Gly Leu Thr Ile Ala Thr Ser Leu Leu	
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tta gcc gct tgt agt gtt ggt gat att gat aaa cag ata gag tta gaa	357
Leu Ala Ala Cys Ser Val Gly Asp Ile Asp Lys Gln Ile Glu Leu Glu	
70 75 80	
caa gaa aaa aag gaa gct gaa aac gct agg gat aga gcg aac aag agt	405
Gln Glu Lys Lys Glu Ala Glu Asn Ala Arg Asp Arg Ala Asn Lys Ser	
85 90 95	
ggg ata gaa ctg gaa cag gaa aaa caa aag acc att aaa gaa caa aaa	453
Gly Ile Glu Leu Glu Gln Glu Lys Gln Lys Thr Ile Lys Glu Gln Lys	
100 105 110	
gat tta gtt aaa aaa gca gaa caa aat tgc caa gaa aat cat ggc caa	501
Asp Leu Val Lys Lys Ala Glu Gln Asn Cys Gln Glu Asn His Gly Gln	

115					120					125										
ttc	ttt	atg	aaa	aaa	tta	gga	att	aag	ggt	ggc	att	gct	ata	gaa	gta	549				
Phe	Phe	Met	Lys	Lys	Leu	Gly	Ile	Lys	Gly	Gly	Ile	Ala	Ile	Glu	Val					
130					135					140					145					
gaa	gct	gaa	tgc	aaa	acc	cct	aaa	cct	gca	aaa	acc	aat	caa	acc	cct	597				
Glu	Ala	Glu	Cys	Lys	Thr	Pro	Lys	Pro	Ala	Lys	Thr	Asn	Gln	Thr	Pro					
150					155					160										
atc	cag	cca	aaa	cac	ctc	ccc	aac	tct	aaa	caa	ccc	cac	tct	caa	aga	645				
Ile	Gln	Pro	Lys	His	Leu	Pro	Asn	Ser	Lys	Gln	Pro	His	Ser	Gln	Arg					
165					170					175										
gga	tca	aaa	gcg	caa	gag	ctt	atc	gct	tat	ttg	caa	aaa	gag	tta	gaa	693				
Gly	Ser	Lys	Ala	Gln	Glu	Leu	Ile	Ala	Tyr	Leu	Gln	Lys	Glu	Leu	Glu					
180					185					190										
tct	ctg	ccc	tat	tca	caa	aaa	gct	atc	gct	aaa	caa	gtg	aat	ttt	tac	741				
Ser	Leu	Pro	Tyr	Ser	Gln	Lys	Ala	Ile	Ala	Lys	Gln	Val	Asn	Phe	Tyr					
195					200					205										
agg	cca	agt	tct	gtc	gct	tat	tta	gaa	cta	gac	cct	aga	gat	ttt	aag	789				
Arg	Pro	Ser	Ser	Val	Ala	Tyr	Leu	Glu	Leu	Asp	Pro	Arg	Asp	Phe	Lys					
210					215					220					225					
gtt	aca	gaa	gaa	tgg	caa	aaa	gaa	aat	cta	aaa	ata	cgc	tct	aaa	gct	837				
Val	Thr	Glu	Glu	Trp	Gln	Lys	Glu	Asn	Leu	Lys	Ile	Arg	Ser	Lys	Ala					
230					235					240										
caa	gct	aaa	atg	ctt	gga	aat	gag	aaa	ccc	aca	agc	cca	cct	ttc	aac	885				
Gln	Ala	Lys	Met	Leu	Gly	Asn	Glu	Lys	Pro	Thr	Ser	Pro	Pro	Phe	Asn					
245					250					255										
ctc	tca	aag	cct	ttt	gtt	cgt	tca	aaa	aat	att	tgc	tgatggttaat				931				
Leu	Ser	Lys	Pro	Phe	Val	Arg	Ser	Lys	Asn	Ile	Cys									
260					265															
aaagaaatag		aagcagttgc		taatactgaa		aagaaagcag		aaaaagmggg		ttaatggttat		991								
agtaaaaagga		tgtaggcata		agaaaataag		aac											1024			

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<211> 269
<212> PRT
<213> Helicobacter pylori
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			20					25					30		
Leu	Asp	Asp	Lys	Val	Gln	Asp	Lys	Ser	Lys	Gln	Ala	Glu	Lys	Glu	Asn
		35				40						45			
Gln	Ile	Asn	Trp	Trp	Lys	Tyr	Ser	Gly	Leu	Thr	Ile	Ala	Thr	Ser	Leu
	50					55					60				
Leu	Leu	Ala	Ala	Cys	Ser	Val	Gly	Asp	Ile	Asp	Lys	Gln	Ile	Glu	Leu
65				70					75					80	
Glu	Gln	Glu	Lys	Lys	Glu	Ala	Glu	Asn	Ala	Arg	Asp	Arg	Ala	Asn	Lys
				85					90					95	

Ser Gly Ile Glu Leu Glu Gln Glu Lys Gln Lys Thr Ile Lys Glu Gln  
 100 105 110  
 Lys Asp Leu Val Lys Lys Ala Glu Gln Asn Cys Gln Glu Asn His Gly  
 115 120 125  
 Gln Phe Met Lys Lys Leu Gly Ile Lys Gly Gly Ile Ala Ile Glu  
 130 135 140  
 Val Glu Ala Glu Cys Lys Thr Pro Lys Pro Ala Lys Thr Asn Gln Thr  
 145 150 155 160  
 Pro Ile Gln Pro Lys His Leu Pro Asn Ser Lys Gln Pro His Ser Gln  
 165 170 175  
 Arg Gly Ser Lys Ala Gln Glu Leu Ile Ala Tyr Leu Gln Lys Glu Leu  
 180 185 190  
 Glu Ser Leu Pro Tyr Ser Gln Lys Ala Ile Ala Lys Gln Val Asn Phe  
 195 200 205  
 Tyr Arg Pro Ser Ser Val Ala Tyr Leu Glu Leu Asp Pro Arg Asp Phe  
 210 215 220  
 Lys Val Thr Glu Glu Trp Gln Lys Glu Asn Leu Lys Ile Arg Ser Lys  
 225 230 235 240  
 Ala Gln Ala Lys Met Leu Gly Asn Glu Lys Pro Thr Ser Pro Pro Phe  
 245 250 255  
 Asn Leu Ser Lys Pro Phe Val Arg Ser Lys Asn Ile Cys  
 260 265

<210> 155  
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 <212> DNA  
 <213> Helicobacter pylori

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 aat ggc gtt ttg gca ggc tat ccg gtg gtg gat ttt aaa gtt acc ctt 104  
 Asn Gly Val Leu Ala Gly Tyr Pro Val Val Asp Phe Lys Val Thr Leu  
 5 10 15  
 tat gat ggg agc tac cat gat gtg gat tct tca gaa atg gcg ttt aaa 152  
 Tyr Asp Gly Ser Tyr His Asp Val Asp Ser Ser Glu Met Ala Phe Lys  
 20 25 30  
 atc gct ggc tct atg gcg ttt aaa gaa gcg agt cgc gcg gct aac ccg 200  
 Ile Ala Gly Ser Met Ala Phe Lys Glu Ala Ser Arg Ala Ala Asn Pro  
 35 40 45 50  
 gtt tta cta gag cct atg atg aaa gtg gaa gtg gaa gtc cct gaa gaa 248  
 Val Leu Leu Glu Pro Met Met Lys Val Glu Val Glu Val Pro Glu Glu  
 55 60 65  
 tac atg ggc gat gtg att ggc gat ttg aat aga aga aga ggg caa atc 296  
 Tyr Met Gly Asp Val Ile Gly Asp Leu Asn Arg Arg Arg Gly Gln Ile  
 70 75 80  
 aat tct atg gac gat aga tta ggc ttg aaa atc gtg aac gct ttt gtg 344  
 Asn Ser Met Asp Asp Arg Leu Gly Leu Lys Ile Val Asn Ala Phe Val

85	90	95	
ccg ttg gtg gaa atg ttt ggc tat tct acg gat tta cga tca gcc acc			392
Pro Leu Val Glu Met Phe Gly Tyr Ser Thr Asp Leu Arg Ser Ala Thr			
100	105	110	
caa ggg cgt ggg act tac tct atg gag ttt gat cat tat ggc gaa gtg			440
Gln Gly Arg Gly Thr Tyr Ser Met Glu Phe Asp His Tyr Gly Glu Val			
115	120	125	130
cct agc aat atc gct aag gaa att gta gaa aag cgc aaa ggc			482
Pro Ser Asn Ile Ala Lys Glu Ile Val Glu Lys Arg Lys Gly			
135	140		
tgatttaatt ataacgctct cttattttta gggggtgtta taggtgctgt tta			535
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Thr Leu Tyr Asp Gly Ser Tyr His Asp Val Asp Ser Ser Glu Met Ala			
20 25 30			
Phe Lys Ile Ala Gly Ser Met Ala Phe Lys Glu Ala Ser Arg Ala Ala			
35 40 45			
Asn Pro Val Leu Leu Glu Pro Met Met Lys Val Glu Val Glu Val Pro			
50 55 60			
Glu Glu Tyr Met Gly Asp Val Ile Gly Asp Leu Asn Arg Arg Arg Gly			
65 70 75 80			
Gln Ile Asn Ser Met Asp Asp Arg Leu Gly Leu Lys Ile Val Asn Ala			
85 90 95			
Phe Val Pro Leu Val Glu Met Phe Gly Tyr Ser Thr Asp Leu Arg Ser			
100 105 110			
Ala Thr Gln Gly Arg Gly Thr Tyr Ser Met Glu Phe Asp His Tyr Gly			
115 120 125			
Glu Val Pro Ser Asn Ile Ala Lys Glu Ile Val Glu Lys Arg Lys Gly			
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		Met Phe	
		1	
tta ggc aac ccg cat tca tcc att ttg aga tta ggc cca acc aca atc			104
Leu Gly Asn Pro His Ser Ser Ile Leu Arg Leu Gly Pro Thr Thr Ile			
5 10 15			

acg	ctt	ctg	cct	gaa	aaa	tcc	acg	cgc	tta	cct	aaa	agg	ttt	tgc	ctg	152
Thr	Leu	Leu	Pro	Glu	Lys	Ser	Thr	Arg	Leu	Pro	Lys	Arg	Phe	Cys	Leu	
	20					25					30					
aaa	cgc	ccc	tgc	ttg	cct	tta	atg	att	tca	ctg	agc	gat	ttt	aaa	ggg	200
Lys	Arg	Pro	Cys	Leu	Pro	Leu	Met	Ile	Ser	Leu	Ser	Asp	Phe	Lys	Gly	
	35				40					45					50	
cgt	ttg	tta	gcc	cct	tta	acc	gca	tta	gtg	ctg	cgg	ccg	tta	tca	aaa	248
Arg	Leu	Leu	Ala	Pro	Leu	Thr	Ala	Leu	Val	Leu	Arg	Pro	Leu	Ser	Lys	
				55					60					65		
agc	aca	tcc	acg	gct	tct	tgc	aac	atc	ctt	ttt	tca	ttg	cgc	aca	atg	296
Ser	Thr	Ser	Thr	Ala	Ser	Cys	Asn	Ile	Leu	Phe	Ser	Leu	Arg	Thr	Met	
			70					75					80			
att	tct	ggc	gct	cca	agc	tcc	att	aag	cgt	ttc	aag	cgt	tgg	tta	cga	344
Ile	Ser	Gly	Ala	Pro	Ser	Ser	Ile	Lys	Arg	Phe	Lys	Arg	Trp	Leu	Arg	
		85					90					95				
ttg	atg	aca	cga	cga	tac	aat	tca	ttc	aca	tcg	ctg	act	gca	aac	ttc	392
Leu	Met	Thr	Arg	Arg	Tyr	Asn	Ser	Phe	Thr	Ser	Leu	Thr	Ala	Asn	Phe	
	100					105					110					
ccg	cca	tct	agc	gcg	act	aaa	ggc	ctt	aaa	tcc	ggg	ggc	aat	acc	ggg	440
Pro	Pro	Ser	Ser	Ala	Thr	Lys	Gly	Leu	Lys	Ser	Gly	Gly	Asn	Thr	Gly	
	115				120					125					130	
aaa	acc	gtg	agc	atc	atc	cat	tca	ggc	cta	tta	cca	gaa	ttt	aaa	aag	488
Lys	Thr	Val	Ser	Ile	Ile	His	Ser	Gly	Leu	Leu	Pro	Glu	Phe	Lys	Lys	
				135				140						145		
ctt	tct	acc	act	ttc	aaa	cgc	tta	atg	agt	ttt	ttc	ttt	ttc	gca	tca	536
Leu	Ser	Thr	Thr	Phe	Lys	Arg	Leu	Met	Ser	Phe	Phe	Phe	Phe	Ala	Ser	
			150					155					160			
gaa	ttg	gtg	tct	ttc	act	tct	tct	ttc	aaa	ctc	tgc	aat	aag	gtg	atc	584
Glu	Leu	Val	Ser	Phe	Thr	Ser	Ser	Phe	Lys	Leu	Cys	Asn	Lys	Val	Ile	
		165					170					175				
aaa	tca	att	tct	tct	aac	aaa	tcc	ttg	atc	gct	tca	ccg	ccc	att	tgc	632
Lys	Ser	Ile	Ser	Ser	Asn	Lys	Ser	Leu	Ile	Ala	Ser	Pro	Pro	Ile	Cys	
	180					185					190					
gct	aca	aag	ccc	ctg	tct	tcg	tat	ctt	cgt	gag	ata	ttt	tgatactgct			681
Ala	Thr	Lys	Pro	Leu	Ser	Ser	Tyr	Leu	Arg	Glu	Ile	Phe				
	195			200						205						
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	35						40					45			
Lys	Gly	Arg	Leu	Leu	Ala	Pro	Leu	Thr	Ala	Leu	Val	Leu	Arg	Pro	Leu
	50						55					60			
Ser	Lys	Ser	Thr	Ser	Thr	Ala	Ser	Cys	Asn	Ile	Leu	Phe	Ser	Leu	Arg
65					70					75					80
Thr	Met	Ile	Ser	Gly	Ala	Pro	Ser	Ser	Ile	Lys	Arg	Phe	Lys	Arg	Trp
				85					90					95	
Leu	Arg	Leu	Met	Thr	Arg	Arg	Tyr	Asn	Ser	Phe	Thr	Ser	Leu	Thr	Ala
			100					105					110		
Asn	Phe	Pro	Pro	Ser	Ser	Ala	Thr	Lys	Gly	Leu	Lys	Ser	Gly	Gly	Asn
		115						120					125		
Thr	Gly	Lys	Thr	Val	Ser	Ile	Ile	His	Ser	Gly	Leu	Leu	Pro	Glu	Phe
	130					135					140				
Lys	Lys	Leu	Ser	Thr	Thr	Phe	Lys	Arg	Leu	Met	Ser	Phe	Phe	Phe	Phe
145					150					155					160
Ala	Ser	Glu	Leu	Val	Ser	Phe	Thr	Ser	Ser	Phe	Lys	Leu	Cys	Asn	Lys
					165				170					175	
Val	Ile	Lys	Ser	Ile	Ser	Ser	Asn	Lys	Ser	Leu	Ile	Ala	Ser	Pro	Pro
		180						185					190		
Ile	Cys	Ala	Thr	Lys	Pro	Leu	Ser	Ser	Tyr	Leu	Arg	Glu	Ile	Phe	
		195					200						205		

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 <221> CDS  
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Gln Cys Gly Glu Arg Asp Phe Arg Gly Leu Phe Phe Gln Ala Ile Arg	
1 5 10 15	
gtg tct aat tac gct aga aat tat caa gtc aaa cac aac ttg gct tac	96
Val Ser Asn Tyr Ala Arg Asn Tyr Gln Val Lys His Asn Leu Ala Tyr	
20 25 30	
tgg ggg gct aaa gat tat tta ggg tgc ggg gct ggg gct gtg ggc tgc	144
Trp Gly Ala Lys Asp Tyr Leu Gly Cys Gly Ala Gly Ala Val Gly Cys	
35 40 45	
gtg gcg aat gag cgc ttt ttt gca aaa aaa ctc ata gaa aac tac atc	192
Val Ala Asn Glu Arg Phe Phe Ala Lys Lys Leu Ile Glu Asn Tyr Ile	
50 55 60	
aaa gac ccc cta caa cgc caa gtt gag acg ctt aat aaa caa gac aaa	240
Lys Asp Pro Leu Gln Arg Gln Val Glu Thr Leu Asn Lys Gln Asp Lys	
65 70 75 80	
cgc tta gaa aag ctg ttt tta ggc ttg agg tgc gtg ctt ggg gtt gag	288
Arg Leu Glu Lys Leu Phe Leu Gly Leu Arg Cys Val Leu Gly Val Glu	
85 90 95	
ctt agt ttc tta gat gaa aat aaa gta aag ttt ttg att gaa gag aac	336



20						25					30						
agc Ser	ggt Gly	tat Tyr	caa Gln	gaa Glu	gtc Val	att Ile	agc Ser	gac Asp	cct Pro	agc Ser	tat Tyr	aag Lys	ggg Gly	caa Gln	ttt Phe	201	
35						40					45						
gtg Val	ggt Val	ttt Phe	agc Ser	atg Met	cct Pro	gag Glu	att Ile	ggg Gly	gtt Val	gtg Val	ggt Gly	gct Ala	aat Asn	tct Ser	aaa Lys	249	
50						55					60						
gat Asp	gat Asp	gaa Glu	tcc Ser	ttt Phe	ttt Phe	tca Ser	tgc Cys	gca Ala	ggg Gly	gtt Val	tta Leu	gcg Ala	cgc Arg	cat His	tac Tyr	297	
70						75					80						
aac Asn	gaa Glu	ttt Phe	ttt Phe	tct Ser	aac Asn	tca Ser	agg Arg	gcg Ala	gat Asp	ttt Phe	agc Ser	ttg Leu	agc Ser	gct Ala	tat Tyr	345	
85						90					95						
ttg Leu	aaa Lys	gag Glu	cgt Arg	ggc Gly	gtt Val	tta Leu	ggg Gly	gtt Val	tgt Cys	ggc Gly	gtt Val	gat Asp	act Thr	agg Arg	agt Ser	393	
100						105					110						
ttg Leu	att Ile	aaa Lys	acc Thr	tta Leu	cgc Arg	cat His	cat His	ggg Gly	tgc Cys	tta Leu	atg Met	atg Met	gtc Val	gct Ala	tcc Ser	441	
115						120					125						
acg Thr	ata Ile	gag Glu	cat His	gac Asp	aaa Lys	aac Asn	aag Lys	ctt Leu	gaa Glu	gaa Glu	att Ile	tta Leu	aaa Lys	aac Asn	gct Ala	489	
130						135					140					145	
cct Pro	aaa Lys	att Ile	tct Ser	cac His	tcc Ser	ccc Pro	cta Leu	gtg Val	tct Ser	agc Ser	gtt Val	tct Ser	acg Thr	cca Pro	aaa Lys	537	
150						155					160						
ata Ile	acc Thr	acg Thr	cac His	cag Gln	cgt Arg	gcg Ala	act Thr	ttt Phe	gat Asp	ttc Phe	aaa Lys	acc Thr	cta Leu	gat Asp	tac Tyr	585	
165						170					175						
aag Lys	cct Pro	ttt Phe	gat Asp	gaa Glu	aaa Lys	acc Thr	tct Ser	cat His	aaa Lys	att Ile	atc Ile	gcg Ala	gtg Val	tta Leu	gac Asp	633	
180						185					190						
ttt Phe	ggg Gly	gct Ala	aag Lys	ggc Gly	aat Asn	att Ile	tta Leu	aac Asn	gag Glu	ctt Leu	caa Gln	aat Asn	gtg Val	ggg Gly	tta Leu	681	
195						200					205						
aaa Lys	gcc Ala	ctt Leu	att Ile	tac Tyr	ccg Pro	cac His	cac His	act Thr	aaa Lys	gct Ala	agc Ser	gag Glu	ctg Leu	att Ile	aaa Lys	729	
210						215					220					225	
gcc Ala	tat Tyr	gaa Glu	aaa Lys	aaa Lys	gaa Glu	att Ile	agc Ser	ggg Gly	att Ile	ttc Phe	ctc Leu	tct Ser	aac Asn	ggg Gly	ccg Pro	777	
230						235					240						
ggc Gly	gat Asp	cct Pro	tta Leu	agc Ser	ttg Leu	cag Gln	caa Gln	gaa Glu	att Ile	ggc Gly	gaa Glu	atc Ile	aaa Lys	caa Gln	ctc Leu	825	
245						250					255						
att Leu	aac Lys	gct Val	aaa Lys	atc Ile	ccc Pro	atg Leu	ctt Leu	ggc Gly	att Ile	tgc Val	tta Leu	ggg Gly	cat Val	caa Lys	ttg Leu	873	



0005913 062901

Ile Asn Ala Lys Ile Pro Met Leu Gly Ile Cys Leu Gly His Gln Leu	
260 265 270	
ctc tct atc gct caa ggc tac cct act tac aag ctc aaa ttt ggt cat	921
Leu Ser Ile Ala Gln Gly Tyr Pro Thr Tyr Lys Leu Lys Phe Gly His	
275 280 285	
cat ggg agc aac cac ccc gtt aaa aac cta aaa aca aac gcc gta gaa	969
His Gly Ser Asn His Pro Val Lys Asn Leu Lys Thr Asn Ala Val Glu	
290 295 300 305	
atc acc gcg caa aac cac aac tat tgc gtc cct gaa gac att gaa gaa	1017
Ile Thr Ala Gln Asn His Asn Tyr Cys Val Pro Glu Asp Ile Glu Glu	
310 315 320	
atc gcc att atc acg cac cgc aat ctt ttt gac aac acc att gag ggc	1065
Ile Ala Ile Ile Thr His Arg Asn Leu Phe Asp Asn Thr Ile Glu Gly	
325 330 335	
gtg cgt tat aaa aac gct ccc att atc tct gtc cag cac cac cca gaa	1113
Val Arg Tyr Lys Asn Ala Pro Ile Ile Ser Val Gln His His Pro Glu	
340 345 350	
agt agc cca ggt cct aaa gag agc cac tat att ttt aaa gaa ttt gtg	1161
Ser Ser Pro Gly Pro Lys Glu Ser His Tyr Ile Phe Lys Glu Phe Val	
355 360 365	
gaa ttg tta aag gat ttt taggggtttt taaaacagcg cttatagaga	1209
Glu Leu Leu Lys Asp Phe	
370 375	
ctgaaaagcg ctttaaaaat agatttaaata ctttttatca aaaaatctcg c	1260
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<212> PRT	
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<400> 162	
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Met Ser Gly Tyr Gln Glu Val Ile Ser Asp Pro Ser Tyr Lys Gly Gln	
35 40 45	
Phe Val Val Phe Ser Met Pro Glu Ile Gly Val Val Gly Ala Asn Ser	
50 55 60	
Lys Asp Asp Glu Ser Phe Phe Ser Cys Ala Gly Val Leu Ala Arg His	
65 70 75 80	
Tyr Asn Glu Phe Phe Ser Asn Ser Arg Ala Asp Phe Ser Leu Ser Ala	
85 90 95	
Tyr Leu Lys Glu Arg Gly Val Leu Gly Val Cys Gly Val Asp Thr Arg	
100 105 110	
Ser Leu Ile Lys Thr Leu Arg His His Gly Cys Leu Met Met Val Ala	
115 120 125	
Ser Thr Ile Glu His Asp Lys Asn Lys Leu Glu Ile Leu Lys Asn	
130 135 140	
Ala Pro Lys Ile Ser His Ser Pro Leu Val Ser Ser Val Ser Thr Pro	
145 150 155 160	

Lys Ile Thr Thr His Gln Arg Ala Thr Phe Asp Phe Lys Thr Leu Asp  
 165 170 175  
 Tyr Lys Pro Phe Asp Glu Lys Thr Ser His Lys Ile Ile Ala Val Leu  
 180 185 190  
 Asp Phe Gly Ala Lys Gly Asn Ile Leu Asn Glu Leu Gln Asn Val Gly  
 195 200 205  
 Leu Lys Ala Leu Ile Tyr Pro His His Thr Lys Ala Ser Glu Leu Ile  
 210 215 220  
 Lys Ala Tyr Glu Lys Lys Glu Ile Ser Gly Ile Phe Leu Ser Asn Gly  
 225 230 235 240  
 Pro Gly Asp Pro Leu Ser Leu Gln Gln Glu Ile Gly Glu Ile Lys Gln  
 245 250 255  
 Leu Ile Asn Ala Lys Ile Pro Met Leu Gly Ile Cys Leu Gly His Gln  
 260 265 270  
 Leu Leu Ser Ile Ala Gln Gly Tyr Pro Thr Tyr Lys Leu Lys Phe Gly  
 275 280 285  
 His His Gly Ser Asn His Pro Val Lys Asn Leu Lys Thr Asn Ala Val  
 290 295 300  
 Glu Ile Thr Ala Gln Asn His Asn Tyr Cys Val Pro Glu Asp Ile Glu  
 305 310 315 320  
 Glu Ile Ala Ile Ile Thr His Arg Asn Leu Phe Asp Asn Thr Ile Glu  
 325 330 335  
 Gly Val Arg Tyr Lys Asn Ala Pro Ile Ser Val Gln His His Pro  
 340 345 350  
 Glu Ser Ser Pro Gly Pro Lys Glu Ser His Tyr Ile Phe Lys Glu Phe  
 355 360 365  
 Val Glu Leu Leu Lys Asp Phe  
 370 375

<210> 163  
 <211> 2790  
 <212> DNA  
 <213> Helicobacter pylori  
 <220>  
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 <222> (116)...(2656)

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 aaagagctat aaaatagcct taaaatacgc gataaaacaa caaaaaggaa taccc atg 118  
 Met  
 1  
 gat att cgc aac gaa ttt tta caa ttt ttt caa aat aaa ggg cat gcc 166  
 Asp Ile Arg Asn Glu Phe Leu Gln Phe Phe Gln Asn Lys Gly His Ala  
 5 10 15  
 gtt tat cct agc atg cct tta gtg cct aat gac gct acc ttg ctt ttt 214  
 Val Tyr Pro Ser Met Pro Leu Val Pro Asn Asp Ala Thr Leu Leu Phe  
 20 25 30  
 acc aat gcc ggc atg gtg caa ttt aaa gat att ttt acc ggg att gtg 262  
 Thr Asn Ala Gly Met Val Gln Phe Lys Asp Ile Phe Thr Gly Ile Val  
 35 40 45  
 cca cgc cct agc att cct aga gcg gca agc tcg caa ttg tgc atg cgc 310  
 Pro Arg Pro Ser Ile Pro Arg Ala Ala Ser Ser Gln Leu Cys Met Arg  
 50 55 60 65

gca ggc ggc aag cat aac gat ttg gaa aat gtc ggt tat acc gca agg Ala Gly Gly Lys His Asn Asp Leu Glu Asn Val Gly Tyr Thr Ala Arg 70 75 80	358
cac cac acg ctt ttt gaa atg cta ggg aat ttc tct ttt ggg gat tat His His Thr Leu Phe Glu Met Leu Gly Asn Phe Ser Phe Gly Asp Tyr 85 90 95	406
ttc aaa gaa gaa gcg atc ttg ttt gcg tgg gaa ttt gta acc aag aat Phe Lys Glu Glu Ala Ile Leu Phe Ala Trp Glu Phe Val Thr Lys Asn 100 105 110	454
tta ggg ttt aag cct aaa gat tta tac atc agc gtg cat gaa aag gac Leu Gly Phe Lys Pro Lys Asp Leu Tyr Ile Ser Val His Glu Lys Asp 115 120 125	502
gat gaa gcc gtt aaa tta tgg gaa aag ttt gtg cct gtt gat agg att Asp Glu Ala Val Lys Leu Trp Glu Lys Phe Val Pro Val Asp Arg Ile 130 135 140 145	550
aaa aaa atg ggc gat aaa gat aat ttt tgg caa atg ggc gat agc ggg Lys Lys Met Gly Asp Lys Asp Asn Phe Trp Gln Met Gly Asp Ser Gly 150 155 160	598
cct tgc ggg cct tgc agt gaa att tac att gat cag ggc gaa aaa cac Pro Cys Gly Pro Cys Ser Glu Ile Tyr Ile Asp Gln Gly Glu Lys His 165 170 175	646
ttt aag ggg agc gag gat tat ttt ggg ggc gag ggc gat agg ttt tta Phe Lys Gly Ser Glu Asp Tyr Phe Gly Gly Glu Gly Asp Arg Phe Leu 180 185 190	694
gaa att tgg aat ctg gtg ttc atg caa tac gaa cgc tct aat gat ggc Glu Ile Trp Asn Leu Val Phe Met Gln Tyr Glu Arg Ser Asn Asp Gly 195 200 205	742
gtt tta tcc ccc ttg cca aag cct agc att gat aca ggc atg gga tta Val Leu Ser Pro Leu Pro Lys Pro Ser Ile Asp Thr Gly Met Gly Leu 210 215 220 225	790
gaa agg gtg caa gcg cta tta gaa cat aag ctc aat aat ttt gat tct Glu Arg Val Gln Ala Leu Leu Glu His Lys Leu Asn Asn Phe Asp Ser 230 235 240	838
tca tta ttt gcg ccc cta atg gaa gaa atc agc gag ctt aca agc cta Ser Leu Phe Ala Pro Leu Met Glu Glu Ile Ser Glu Leu Thr Ser Leu 245 250 255	886
gat tat gcg agc gag ttc cag cca agc ttt agg gta gtg gcc gat cac Asp Tyr Ala Ser Glu Phe Gln Pro Ser Phe Arg Val Val Ala Asp His 260 265 270	934
gca aga gcg gta gca ttc ttg ctc gct caa ggg gtg cat ttc aat aag Ala Arg Ala Val Ala Phe Leu Leu Ala Gln Gly Val His Phe Asn Lys 275 280 285	982
gaa ggc cgt ggc tat gtt tta agg cgc att tta agg cga gcc tta agg Glu Gly Arg Gly Tyr Val Leu Arg Arg Ile Leu Arg Arg Ala Leu Arg	1030



Lys 530	Lys	Ala	Leu	Lys	Lys 535	Gly	Asp	Gln	Val	Ile 540	Ala	Gln	Val	Ser	Asp 545	
gag	cgc	ttt	gaa	atc	gcc	aaa	cac	cat	agt	gcg	act	cat	tta	ttg	cag	1798
Glu	Arg	Phe	Glu	Ile 550	Ala	Lys	His	His	Ser 555	Ala	Thr	His	Leu	Leu	Gln 560	
agc	gct	tta	aga	gaa	gtt	tta	ggc	tcg	cat	gtg	agt	caa	gcg	ggg	agt	1846
Ser	Ala	Leu	Arg	Glu	Val	Leu	Gly	Ser	His	Val	Ser	Gln	Ala	Gly	Ser 575	
tta	gtg	gaa	tcc	aag	cga	ttg	cgc	ttt	gat	ttc	tcg	cat	gct	aaa	gcg	1894
Leu	Val	Glu	Ser	Lys	Arg	Leu	Arg	Phe	Asp	Phe	Ser	His	Ala	Lys	Ala 590	
ctc	aat	gat	gaa	gag	cta	gaa	aaa	gta	gaa	gat	tta	gtc	aac	gct	caa	1942
Leu	Asn	Asp	Glu	Glu	Leu	Glu	Lys	Val	Glu	Asp	Leu	Val	Asn	Ala	Gln 605	
att	ttc	aag	cac	cta	aat	agc	cag	gtg	gag	cat	atg	cct	tta	aac	caa	1990
Ile	Phe	Lys	His	Leu	Asn	Ser	Gln	Val	Glu	His	Met	Pro	Leu	Asn	Gln 625	
gcc	aaa	gat	aag	gga	gcg	tta	gcg	tta	ttc	agt	gaa	aaa	tac	gct	gaa	2038
Ala	Lys	Asp	Lys	Gly	Ala	Leu	Ala	Leu	Phe	Ser	Glu	Lys	Tyr	Ala	Glu 640	
aat	gtg	cgg	gtg	gtg	agc	ttt	aaa	gaa	gcg	tcc	att	gaa	ttg	tgt	ggg	2086
Asn	Val	Arg	Val	Val	Ser	Phe	Lys	Glu	Ala	Ser	Ile	Glu	Leu	Cys	Gly 655	
ggc	att	cat	gtg	gaa	aat	act	ggg	ctt	att	ggg	ggg	ttt	agg	att	gta	2134
Gly	Ile	His	Val	Glu	Asn	Thr	Gly	Leu	Ile	Gly	Gly	Phe	Arg	Ile	Val 670	
aaa	gaa	agc	ggg	gtg	agt	agt	ggg	gtc	aga	cgc	att	gaa	gcg	gtg	tgc	2182
Lys	Glu	Ser	Gly	Val	Ser	Ser	Gly	Val	Arg	Arg	Ile	Glu	Ala	Val	Cys 685	
ggg	aaa	gcc	ttt	tac	caa	ctg	gct	aaa	gaa	gaa	aat	aaa	gag	ctt	aaa	2230
Gly	Lys	Ala	Phe	Tyr	Gln	Leu	Ala	Lys	Glu	Glu	Asn	Lys	Glu	Leu	Lys 705	
aac	gct	aag	act	tta	ttg	aaa	aat	aac	gat	gtg	atc	gcc	ggt	atc	aat	2278
Asn	Ala	Lys	Thr	Leu	Leu	Lys	Asn	Asn	Asp	Val	Ile	Ala	Gly	Ile	Asn 720	
aag	ctt	aaa	gag	agc	gtg	aaa	aac	agc	caa	aaa	gcc	ccc	gtt	tct	atg	2326
Lys	Leu	Lys	Glu	Ser	Val	Lys	Asn	Ser	Gln	Lys	Ala	Pro	Val	Ser	Met 735	
gat	tta	ccg	gtt	gaa	aaa	atc	cat	ggc	gtg	aat	ttg	gtg	gtg	ggc	gta	2374
Asp	Leu	Pro	Val	Glu	Lys	Ile	His	Gly	Val	Asn	Leu	Val	Val	Gly	Val 750	
gtg	gaa	caa	ggc	gac	att	aaa	gaa	atg	att	gac	cga	ttg	aaa	agt	aag	2422
Val	Glu	Gln	Gly	Asp	Ile	Lys	Glu	Met	Ile	Asp	Arg	Leu	Lys	Ser	Lys 765	



225					230				235				240			
Ser	Ser	Leu	Phe	Ala	Pro	Leu	Met	Glu	Glu	Ile	Ser	Glu	Leu	Thr	Ser	
				245					250					255		
Leu	Asp	Tyr	Ala	Ser	Glu	Phe	Gln	Pro	Ser	Phe	Arg	Val	Val	Ala	Asp	
			260					265					270			
His	Ala	Arg	Ala	Val	Ala	Phe	Leu	Leu	Ala	Gln	Gly	Val	His	Phe	Asn	
		275					280					285				
Lys	Glu	Gly	Arg	Gly	Tyr	Val	Leu	Arg	Arg	Ile	Leu	Arg	Arg	Ala	Leu	
	290					295					300					
Arg	His	Gly	Tyr	Leu	Met	Gly	Leu	Lys	Glu	Ala	Phe	Leu	Tyr	Lys	Val	
305					310					315					320	
Val	Gly	Val	Val	Cys	Glu	Gln	Phe	Ala	Asn	Thr	His	Ala	Tyr	Leu	Lys	
				325					330					335		
Glu	Ser	Lys	Glu	Met	Val	Val	Lys	Glu	Cys	Phe	Glu	Glu	Glu	Glu	His	
			340					345					350			
Phe	Leu	Glu	Thr	Leu	Glu	Ser	Gly	Met	Glu	Leu	Phe	Asn	Leu	Ser	Leu	
		355					360					365				
Lys	His	Leu	Asn	Glu	Asn	Lys	Ile	Phe	Asp	Gly	Lys	Ile	Ala	Phe	Lys	
	370					375					380					
Leu	Tyr	Asp	Thr	Phe	Gly	Phe	Pro	Leu	Asp	Leu	Thr	Asn	Asp	Met	Leu	
385					390					395					400	
Arg	Ser	His	Gly	Ala	Cys	Ala	Asp	Met	Gln	Gly	Phe	Glu	Leu	Cys	Met	
				405					410					415		
Gln	Glu	Gln	Val	Lys	Arg	Ser	Lys	Ala	Ser	Trp	Lys	Gly	Lys	Gln	Asn	
			420					425					430			
Asn	Ala	Asp	Phe	Ser	Ala	Ile	Leu	Asn	Ala	Tyr	Ala	Pro	Asn	Val	Phe	
		435					440					445				
Val	Gly	Tyr	Glu	Thr	Thr	Glu	Cys	Ser	Ala	Lys	Val	Leu	Gly	Phe	Phe	
	450					455					460					
Asp	Ser	Asp	Phe	Lys	Glu	Ile	Thr	Asp	Ala	Asn	Pro	Asn	Gln	Glu	Val	
465					470					475					480	
Trp	Val	Leu	Leu	Glu	Lys	Thr	Pro	Phe	Tyr	Ala	Glu	Gly	Gly	Gly	Ala	
				485					490				495			
Ile	Gly	Asp	Arg	Gly	Ala	Leu	Phe	Lys	Asp	Asn	Gly	Glu	Val	Ala	Ile	
			500					505					510			
Val	Leu	Asp	Thr	Lys	Asn	Phe	Phe	Gly	Leu	Asn	Phe	Ser	Leu	Leu	Glu	
		515					520					525				
Ile	Lys	Lys	Ala	Leu	Lys	Lys	Gly	Asp	Gln	Val	Ile	Ala	Gln	Val	Ser	
	530					535					540					
Asp	Glu	Arg	Phe	Glu	Ile	Ala	Lys	His	His	Ser	Ala	Thr	His	Leu	Leu	
545					550					555					560	
Gln	Ser	Ala	Leu	Arg	Glu	Val	Leu	Gly	Ser	His	Val	Ser	Gln	Ala	Gly	
				565					570					575		
Ser	Leu	Val	Glu	Ser	Lys	Arg	Leu	Arg	Phe	Asp	Phe	Ser	His	Ala	Lys	
			580													





Leu	Gln	Phe	Met	Asp	Lys	Lys	Ser	Asp	Asn	Pro	Gln	Ala	Asn	Ala	Met		
			105					110					115				
caa	gat	agt	ata	atg	cat	gag	aat	tcc	aac	aac	gct	tat	ccc	gct	aat	498	
Gln	Asp	Ser	Ile	Met	His	Glu	Asn	Ser	Asn	Asn	Ala	Tyr	Pro	Ala	Asn		
			120				125					130					
cat	aac	gct	ccc	agc	caa	gat	cct	ttt	aac	caa	gct	tat	gcg	caa	aac	546	
His	Asn	Ala	Pro	Ser	Gln	Asp	Pro	Phe	Asn	Gln	Ala	Tyr	Ala	Gln	Asn		
			135			140					145						
gct	tac	gct	aaa	gag	aat	tta	caa	gca	cag	ccg	tcc	aag	tat	caa	aac	594	
Ala	Tyr	Ala	Lys	Glu	Asn	Leu	Gln	Ala	Gln	Pro	Ser	Lys	Tyr	Gln	Asn		
			150			155				160					165		
agc	gtg	cct	gaa	atc	aat	att	gat	gaa	gaa	gaa	atc	ccc	ttt			636	
Ser	Val	Pro	Glu	Ile	Asn	Ile	Asp	Glu	Glu	Glu	Ile	Pro	Phe				
				170					175								
taaggggttaa	aattaaggag	acattatgga	aagaaaaacgc	tattcaaaaac	gctattgcaa	696											
atacactgaa	gctaaaatca	gctt				720											

<210> 166  
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 <212> PRT  
 <213> Helicobacter pylori

Met	Phe	Asn	Lys	Val	Ile	Met	Val	Gly	Arg	Leu	Thr	Arg	Asn	Val	Glu		
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Leu	Lys	Tyr	Leu	Pro	Ser	Gly	Ser	Ala	Ala	Ala	Thr	Ile	Gly	Leu	Ala		
			20					25				30					
Thr	Ser	Arg	Arg	Phe	Lys	Lys	Gln	Asp	Gly	Thr	Leu	Gly	Glu	Glu	Val		
		35					40					45					
Cys	Phe	Ile	Asp	Ala	Arg	Leu	Phe	Gly	Arg	Thr	Ala	Glu	Ile	Ala	Asn		
		50				55				60							
Gln	Tyr	Leu	Ser	Lys	Gly	Ser	Ser	Val	Leu	Ile	Glu	Gly	Arg	Leu	Thr		
65				70				75						80			
Tyr	Glu	Ser	Trp	Met	Asp	Gln	Thr	Gly	Lys	Lys	Asn	Ser	Arg	His	Thr		
			85					90						95			
Ile	Thr	Ala	Asp	Ser	Leu	Gln	Phe	Met	Asp	Lys	Lys	Ser	Asp	Asn	Pro		
			100					105					110				
Gln	Ala	Asn	Ala	Met	Gln	Asp	Ser	Ile	Met	His	Glu	Asn	Ser	Asn	Asn		
		115				120						125					
Ala	Tyr	Pro	Ala	Asn	His	Asn	Ala	Pro	Ser	Gln	Asp	Pro	Phe	Asn	Gln		
		130				135					140						
Ala	Tyr	Ala	Gln	Asn	Ala	Tyr	Ala	Lys	Glu	Asn	Leu	Gln	Ala	Gln	Pro		
145				150					155						160		
Ser	Lys	Tyr	Gln	Asn	Ser	Val	Pro	Glu	Ile	Asn	Ile	Asp	Glu	Glu	Glu		
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Ile Pro Phe

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106690"ET65660

<221> CDS  
 <222> (91)...(879)

<400> 167

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aactttttaaa aaaggctgaa tgaaagaata atg aaa tta aaa tct ttt ggg gtt	114
Met Lys Leu Lys Ser Phe Gly Val	
1 5	
ttt gga aat ccc att aag cat tcc aaa tcg ccc tta atc cat aac gct	162
Phe Gly Asn Pro Ile Lys His Ser Lys Ser Pro Leu Ile His Asn Ala	
10 15 20	
tgt ttt tta act ttt caa aaa gaa tta agg ttt ttg ggg cat tac cac	210
Cys Phe Leu Thr Phe Gln Lys Glu Leu Arg Phe Leu Gly His Tyr His	
25 30 35 40	
ccc ata tta ctc cct tta gaa agc cac atc aaa agc gag ttt ttg cat	258
Pro Ile Leu Leu Pro Leu Glu Ser His Ile Lys Ser Glu Phe Leu His	
45 50 55	
ttg gga ttg agt ggg gct aat gta acc tta ccc ttt aaa gaa agg gcg	306
Leu Gly Leu Ser Gly Ala Asn Val Thr Leu Pro Phe Lys Glu Arg Ala	
60 65 70	
ttt caa gtt tgc gat aaa atc aaa ggt atc gcg ctt gaa tgc gga gcg	354
Phe Gln Val Cys Asp Lys Ile Lys Gly Ile Ala Leu Glu Cys Gly Ala	
75 80 85	
gtc aat acg ctt gtt tta gaa aat gat gag ctt gtg ggt tac aat acc	402
Val Asn Thr Leu Val Leu Glu Asn Asp Glu Leu Val Gly Tyr Asn Thr	
90 95 100	
gac gct tta ggg ttt tat ctt tct tta aag caa aaa aac tat caa aac	450
Asp Ala Leu Gly Phe Tyr Leu Ser Leu Lys Gln Lys Asn Tyr Gln Asn	
105 110 115 120	
gct ttg att tta gga gct ggg ggg agc gct aaa gcc cta gcg tgt gaa	498
Ala Leu Ile Leu Gly Ala Gly Gly Ser Ala Lys Ala Leu Ala Cys Glu	
125 130 135	
ttg aaa aaa caa ggc tta caa gtg agc gtg ttg aac cgc tct tct agg	546
Leu Lys Lys Gln Gly Leu Gln Val Ser Val Leu Asn Arg Ser Ser Arg	
140 145 150	
gga ttg gat ttt ttc caa cgc ctg ggc tgt gat tgt ttt atg gag cct	594
Gly Leu Asp Phe Phe Gln Arg Leu Gly Cys Asp Cys Phe Met Glu Pro	
155 160 165	
cct aaa agc gct ttt gat ttg att att aac gcc act tca gcg agt ttg	642
Pro Lys Ser Ala Phe Asp Leu Ile Ile Asn Ala Thr Ser Ala Ser Leu	
170 175 180	
cat aac gaa ttg cct ttg aat aaa gag gtt ttg aaa ggg tat ttt aaa	690
His Asn Glu Leu Pro Leu Asn Lys Glu Val Leu Lys Gly Tyr Phe Lys	
185 190 195 200	
gag ggc aag ctc gct tat gat ttg gcg tat ggg ttt tta acg ccc ttt	738
Glu Gly Lys Leu Ala Tyr Asp Leu Ala Tyr Gly Phe Leu Thr Pro Phe	

205

210

215

ttg tct tta gcc aaa gag tta aaa acc cct ttt caa gac gga aaa gac 786  
 Leu Ser Leu Ala Lys Glu Leu Lys Thr Pro Phe Gln Asp Gly Lys Asp  
                   220                                   225                                   230

atg ctc atc tat caa gct gct tta agt ttt gaa aaa ttc agc gct tct 834  
 Met Leu Ile Tyr Gln Ala Ala Leu Ser Phe Glu Lys Phe Ser Ala Ser  
                   235                                   240                                   245

caa atc cct tat tca aaa gcg ttt gaa gtc atg cga agt gtt ttt 879  
 Gln Ile Pro Tyr Ser Lys Ala Phe Glu Val Met Arg Ser Val Phe  
                   250                                   255                                   260

tgatgcaagg gtttttaaga agcctgtttt ttgggggttaa aaagatccct aaaccattcg 939  
 ctctcttagt agaaaagggc gtttttaaaag aagcgcttga attgaaaaag g 990

&lt;210&gt; 168

&lt;211&gt; 263

&lt;212&gt; PRT

&lt;213&gt; Helicobacter pylori

&lt;400&gt; 168

Met Lys Leu Lys Ser Phe Gly Val Phe Gly Asn Pro Ile Lys His Ser  
   1                  5                  10                  15  
 Lys Ser Pro Leu Ile His Asn Ala Cys Phe Leu Thr Phe Gln Lys Glu  
                   20                  25                  30  
 Leu Arg Phe Leu Gly His Tyr His Pro Ile Leu Leu Pro Leu Glu Ser  
                   35                  40                  45  
 His Ile Lys Ser Glu Phe Leu His Leu Gly Leu Ser Gly Ala Asn Val  
   50                  55                  60  
 Thr Leu Pro Phe Lys Glu Arg Ala Phe Gln Val Cys Asp Lys Ile Lys  
   65                  70                  75                  80  
 Gly Ile Ala Leu Glu Cys Gly Ala Val Asn Thr Leu Val Leu Glu Asn  
                   85                  90                  95  
 Asp Glu Leu Val Gly Tyr Asn Thr Asp Ala Leu Gly Phe Tyr Leu Ser  
                   100                  105                  110  
 Leu Lys Gln Lys Asn Tyr Gln Asn Ala Leu Ile Leu Gly Ala Gly Gly  
                   115                  120                  125  
 Ser Ala Lys Ala Leu Ala Cys Glu Leu Lys Lys Gln Gly Leu Gln Val  
   130                  135                  140  
 Ser Val Leu Asn Arg Ser Ser Arg Gly Leu Asp Phe Phe Gln Arg Leu  
   145                  150                  155                  160  
 Gly Cys Asp Cys Phe Met Glu Pro Pro Lys Ser Ala Phe Asp Leu Ile  
                   165                  170                  175  
 Ile Asn Ala Thr Ser Ala Ser Leu His Asn Glu Leu Pro Leu Asn Lys  
                   180                  185                  190  
 Glu Val Leu Lys Gly Tyr Phe Lys Glu Gly Lys Leu Ala Tyr Asp Leu  
                   195                  200                  205  
 Ala Tyr Gly Phe Leu Thr Pro Phe Leu Ser Leu Ala Lys Glu Leu Lys  
                   210                  215                  220  
 Thr Pro Phe Gln Asp Gly Lys Asp Met Leu Ile Tyr Gln Ala Ala Leu  
   225                  230                  235                  240  
 Ser Phe Glu Lys Phe Ser Ala Ser Gln Ile Pro Tyr Ser Lys Ala Phe  
                   245                  250                  255  
 Glu Val Met Arg Ser Val Phe  
                   260

&lt;210&gt; 169

090901.3.062901

<211> 1080  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (47)...(1033)

<400> 169

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Met Ser Ala	
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tat atc att gaa acc ctg att aaa att ttg att tta gtc gct gtt ttt	103
Tyr Ile Ile Glu Thr Leu Ile Lys Ile Leu Ile Leu Val Ala Val Phe	
5 10 15	
tcg gct tta gga ggc ttt gcc act tat att gaa agg aaa gtg tta gcc	151
Ser Ala Leu Gly Gly Phe Ala Thr Tyr Ile Glu Arg Lys Val Leu Ala	
20 25 30 35	
tat ttc caa cgc cgt tta ggg cct tgt tat gtg ggg cct ttt ggg ctt	199
Tyr Phe Gln Arg Arg Leu Gly Pro Cys Tyr Val Gly Pro Phe Gly Leu	
40 45 50	
ttg caa gtc gca gca gac ggc att aag ctt ttc act aaa gaa gac att	247
Leu Gln Val Ala Ala Asp Gly Ile Lys Leu Phe Thr Lys Glu Asp Ile	
55 60 65	
atc cct caa ggc gcg aac aaa ttc att ttc acg cta gcg ccc att att	295
Ile Pro Gln Gly Ala Asn Lys Phe Ile Phe Thr Leu Ala Pro Ile Ile	
70 75 80	
gcg atg gtg agt gcg ttt gtg tcc atg gcg cct atc ccc ttt ttc cct	343
Ala Met Val Ser Ala Phe Val Ser Met Ala Pro Ile Pro Phe Phe Pro	
85 90 95	
aat ttc act ctg ttt ggc tat gag atc aag ccc ctt att tct gac atc	391
Asn Phe Thr Leu Phe Gly Tyr Glu Ile Lys Pro Leu Ile Ser Asp Ile	
100 105 110 115	
aac att ggc ttt ttg ttt ttc tta gcc gtg ggt tcg gca ggg att tat	439
Asn Ile Gly Phe Leu Phe Phe Leu Ala Val Gly Ser Ala Gly Ile Tyr	
120 125 130	
gcg cct att tta gcc ggg ctt gcc tct aat aac aaa tac tct tta att	487
Ala Pro Ile Leu Ala Gly Leu Ala Ser Asn Asn Lys Tyr Ser Leu Ile	
135 140 145	
ggc tcc gca aga gcg acg atc caa ctg ctc agc ttt gaa gtg gtc agc	535
Gly Ser Ala Arg Ala Thr Ile Gln Leu Leu Ser Phe Glu Val Val Ser	
150 155 160	
act tta acc att cta gcc ccc tta atg gtg gta gga tcg ctc tct tta	583
Thr Leu Thr Ile Leu Ala Pro Leu Met Val Val Gly Ser Leu Ser Leu	
165 170 175	
gtg gaa atc aat cat tac caa agc ggt ggg ttt tta gac tgg ctt gtg	631
Val Glu Ile Asn His Tyr Gln Ser Gly Gly Phe Leu Asp Trp Leu Val	

180	185	190	195	
ttt aag cag cct cta gcg ttt gtt ttg ttt ttg atc gca agt tat gcc				679
Phe Lys Gln Pro	Leu Ala Phe Val	Leu Phe Leu Ile	Ala Ser Tyr Ala	
	200	205	210	
gaa ttg aat cga acc ccc ttt gac ttg cta gag cat gaa gcc gag atc				727
Glu Leu Asn Arg Thr	Pro Phe Asp	Leu Leu Glu His	Glu Ala Glu Ile	
	215	220	225	
gtg gcg ggg tat tgc acc gaa tac agc ggc ttg aaa tgg ggc atg ttc				775
Val Ala Gly Tyr Cys Thr	Glu Tyr Ser	Gly Leu Lys	Trp Gly Met Phe	
	230	235	240	
ttt tta gcg gaa tac gcg cat tta ttc gct ttt tct ttt gtg att tct				823
Phe Leu Ala Glu Tyr	Ala His Leu Phe	Ala Phe Ser	Phe Val Ile Ser	
	245	250	255	
att gtg ttt ttt ggc ggg ttt aac gca tgg ggc ttt atc cct gga ggc				871
Ile Val Phe Phe Gly Gly	Phe Asn Ala	Trp Gly Phe	Ile Pro Gly Gly	
	260	265	270	275
ata gcg att ttg att aaa gcg ggc ttt ttt gtc ttt tta tcc atg tgg				919
Ile Ala Ile Leu Ile Lys	Ala Gly Phe	Phe Val Phe	Leu Ser Met Trp	
	280	285	290	
gtt aga gcg act tat ccg cat gtg cgc cca gac caa ctg atg gat atg				967
Val Arg Ala Thr Tyr	Pro His Val	Arg Pro Asp	Gln Leu Met Asp Met	
	295	300	305	
tgc tgg aaa atc atg ctg cct tta gcg tta ttg aac att gtg cta acg				1015
Cys Trp Lys Ile Met Leu	Pro Leu Ala	Leu Leu Asn	Ile Val Leu Thr	
	310	315	320	
ggc att atc att tta att taaaggaggt tttatggcca aacaagaata				1063
Gly Ile Ile Ile Leu Ile				
	325			
caagcaactt cctaaac				1080
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<212>	PRT			
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1 5 10 15				
Ala Val Phe Ser Ala Leu Gly Gly Phe Ala Thr Tyr Ile Glu Arg Lys				
20 25 30				
Val Leu Ala Tyr Phe Gln Arg Arg Leu Gly Pro Cys Tyr Val Gly Pro				
35 40 45				
Phe Gly Leu Leu Gln Val Ala Ala Asp Gly Ile Lys Leu Phe Thr Lys				
50 55 60				
Glu Asp Ile Ile Pro Gln Gly Ala Asn Lys Phe Ile Phe Thr Leu Ala				
65 70 75 80				
Pro Ile Ile Ala Met Val Ser Ala Phe Val Ser Met Ala Pro Ile Pro				
85 90 95				
Phe Phe Pro Asn Phe Thr Leu Phe Gly Tyr Glu Ile Lys Pro Leu Ile				

100 105 110  
 Ser Asp Ile Asn Ile Gly Phe Leu Phe Phe Leu Ala Val Gly Ser Ala  
 115 120 125  
 Gly Ile Tyr Ala Pro Ile Leu Ala Gly Leu Ala Ser Asn Asn Lys Tyr  
 130 135 140  
 Ser Leu Ile Gly Ser Ala Arg Ala Thr Ile Gln Leu Leu Ser Phe Glu  
 145 150 155 160  
 Val Val Ser Thr Leu Thr Ile Leu Ala Pro Leu Met Val Val Gly Ser  
 165 170 175  
 Leu Ser Leu Val Glu Ile Asn His Tyr Gln Ser Gly Gly Phe Leu Asp  
 180 185 190  
 Trp Leu Val Phe Lys Gln Pro Leu Ala Phe Val Leu Phe Leu Ile Ala  
 195 200 205  
 Ser Tyr Ala Glu Leu Asn Arg Thr Pro Phe Asp Leu Leu Glu His Glu  
 210 215 220  
 Ala Glu Ile Val Ala Gly Tyr Cys Thr Glu Tyr Ser Gly Leu Lys Trp  
 225 230 235 240  
 Gly Met Phe Phe Leu Ala Glu Tyr Ala His Leu Phe Ala Phe Ser Phe  
 245 250 255  
 Val Ile Ser Ile Val Phe Phe Gly Gly Phe Asn Ala Trp Gly Phe Ile  
 260 265 270  
 Pro Gly Gly Ile Ala Ile Leu Ile Lys Ala Gly Phe Phe Val Phe Leu  
 275 280 285  
 Ser Met Trp Val Arg Ala Thr Tyr Pro His Val Arg Pro Asp Gln Leu  
 290 295 300  
 Met Asp Met Cys Trp Lys Ile Met Leu Pro Leu Ala Leu Leu Asn Ile  
 305 310 315 320  
 Val Leu Thr Gly Ile Ile Ile Leu Ile  
 325

<210> 171  
 <211> 1280  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (48)...(1226)

<400> 171  
 taaggataaa atcaagcgat tagcccgaat tttaagagag tattaag atg aat aaa 56  
 Met Asn Lys  
 1  
  
 aaa gcg tat ttt ggg gag ttt gga ggg agt ttt gtt tcg gag ttg tta 104  
 Lys Ala Tyr Phe Gly Glu Phe Gly Gly Ser Phe Val Ser Glu Leu Leu  
 5 10 15  
  
 gtg cct gca tta aga gaa tta gaa cag gcg ttt gat gcg tgt ttg aaa 152  
 Val Pro Ala Leu Arg Glu Leu Glu Gln Ala Phe Asp Ala Cys Leu Lys  
 20 25 30 35  
  
 gat gaa aaa ttc caa aaa gaa tat ttt cgt ctt tta aag gat ttt gtg 200  
 Asp Glu Lys Phe Gln Lys Glu Tyr Phe Arg Leu Leu Lys Asp Phe Val  
 40 45 50  
  
 ggc cgt cct agc cct tta acc ttg tgt caa aat atc gtt tct aac cct 248  
 Gly Arg Pro Ser Pro Leu Thr Leu Cys Gln Asn Ile Val Ser Asn Pro  
 55 60 65



			295					300						305						
ggg cca gaa cac agc tat tta aaa gaa agt ggg cgt gcg gtt tat gaa	Gly Pro Glu His Ser Tyr Leu Lys Glu Ser Gly Arg Ala Val Tyr Glu	1016																		
	310 315 320																			
agc gca agc gat gct gaa gcg cta gaa gcc ttc aag ttg ttg tgc caa	Ser Ala Ser Asp Ala Glu Ala Leu Glu Ala Phe Lys Leu Leu Cys Gln	1064																		
	325 330 335																			
aaa gaa ggc att atc cca gcg cta gaa agc tca cac gcc tta gcg tat	Lys Glu Gly Ile Ile Pro Ala Leu Glu Ser Ser His Ala Leu Ala Tyr	1112																		
	340 345 350 355																			
gcc tta aag ctg gct caa aaa tgc gaa gaa gaa agc atc atc gta gtg	Ala Leu Lys Leu Ala Gln Lys Cys Glu Glu Glu Ser Ile Ile Val Val	1160																		
	360 365 370																			
aat tta agc ggc aga ggg gat aag gat tta agc acc gtt tat aac gct	Asn Leu Ser Gly Arg Gly Asp Lys Asp Leu Ser Thr Val Tyr Asn Ala	1208																		
	375 380 385																			
tta aaa gga ggt tta aaa tgaggatatca aaacatgttt gaaaccttaa	Leu Lys Gly Leu Lys	1256																		
	390																			
aaaaaacacga aaaaatggcg ttta		1280																		
<210>	172																			
<211>	393																			
<212>	PRT																			
<213>	Helicobacter pylori																			
<400>	172																			
Met Asn Lys Lys Ala Tyr Phe Gly Glu Phe Gly Gly Ser Phe Val Ser	1 5 10 15																			
Glu Leu Leu Val Pro Ala Leu Arg Glu Leu Glu Gln Ala Phe Asp Ala	20 25 30																			
Cys Leu Lys Asp Glu Lys Phe Gln Lys Glu Tyr Phe Arg Leu Leu Lys	35 40 45																			
Asp Phe Val Gly Arg Pro Ser Pro Leu Thr Leu Cys Gln Asn Ile Val	50 55 60																			
Ser Asn Pro Lys Val Lys Leu Tyr Leu Lys Arg Glu Asp Leu Ile His	65 70 75 80																			
Gly Gly Ala His Lys Thr Asn Gln Ala Leu Gly Gln Ala Leu Leu Ala	85 90 95																			
Lys Lys Met Gly Lys Thr Arg Ile Ile Ala Glu Thr Gly Ala Gly Gln	100 105 110																			
His Gly Val Ala Thr Ala Ile Ala Cys Ala Leu Leu Asn Leu Lys Cys	115 120 125																			
Val Val Phe Met Gly Ser Lys Asp Ile Lys Arg Gln Glu Met Asn Val	130 135 140																			
Phe Arg Met His Leu Leu Gly Ala Glu Val Arg Glu Val Asn Ser Gly	145 150 155 160																			
Ser Ala Thr Leu Lys Asp Ala Val Asn Glu Ala Leu Arg Asp Trp Ala	165 170 175																			
Ser Ser Tyr Lys Asp Thr His Tyr Leu Leu Gly Thr Ala Ala Gly Pro	180 185 190																			
His Pro Tyr Pro Thr Met Val Lys Thr Phe Gln Lys Met Ile Gly Asp																				



195	200	205
Glu Val Lys Ser Gln Ile Leu	Glu Lys Glu Asn Arg Leu	Pro Asp Tyr
210	215	220
Val Ile Ala Cys Val Gly	Gly Ser Asn Ala Ile	Gly Ile Phe Ser
225	230	235
Ala Phe Leu Asn Asp Lys	Glu Val Lys Leu Ile	Gly Val Glu Pro Ala
245	250	255
Gly Leu Gly Leu Glu Thr	Asn Lys His Gly Ala Thr	Leu Asn Lys Gly
260	265	270
Arg Val Gly Ile Leu His	Gly Asn Lys Thr Tyr Leu	Leu Gln Asp Asp
275	280	285
Glu Gly Gln Ile Ala Glu	Ser His Ser Ile Ser Ala	Gly Leu Asp Tyr
290	295	300
Pro Gly Val Gly Pro Glu	Ser His Ser Tyr Leu Lys	Glu Ser Gly Arg Ala
305	310	315
Val Tyr Glu Ser Ala Ser	Asp Ala Glu Ala Leu Glu	Ala Phe Lys Leu
325	330	335
Leu Cys Gln Lys Glu Gly	Ile Ile Pro Ala Leu Glu	Ser Ser His Ala
340	345	350
Leu Ala Tyr Ala Leu Lys	Leu Ala Gln Lys Cys Glu	Glu Glu Ser Ile
355	360	365
Ile Val Val Asn Leu Ser	Gly Arg Gly Asp Lys Asp	Leu Ser Thr Val
370	375	380
Tyr Asn Ala Leu Lys Gly	Gly Leu Lys	
385	390	

<210> 173  
 <211> 559  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (31)...(513)

<400> 173	
caggtagctt tgggcgagaa aggagagagc atg aat gtc aaa aat cgt ttg agc	54
Met Asn Val Lys Asn Arg Leu Ser	
1 5	
gat tgg gaa tat caa tgg gca gtg gct cta gtc tat acg ata tgt atc	102
Asp Trp Glu Tyr Gln Trp Ala Val Ala Leu Val Tyr Thr Ile Cys Ile	
10 15 20	
tcc ata aac gct agg att ttt tat gac ata gat ggt tca gct agc gat	150
Ser Ile Asn Ala Arg Ile Phe Tyr Asp Ile Asp Gly Ser Ala Ser Asp	
25 30 35 40	
tcg att ttt gac cct aaa aat agc tat tat atg tgg cta gtg ggt cta	198
Ser Ile Phe Asp Pro Lys Asn Ser Tyr Tyr Met Trp Leu Val Gly Leu	
45 50 55	
ata gcg gct ttg ttg tct aac ctt tta ttt gac cca cga ggt agg gat	246
Ile Ala Ala Leu Leu Ser Asn Leu Leu Phe Asp Pro Arg Gly Arg Asp	
60 65 70	
tgt tat aaa tct ttc caa gta aga tac cct agg ttt ctc aaa gcc att	294
Cys Tyr Lys Ser Phe Gln Val Arg Tyr Pro Arg Phe Leu Lys Ala Ile	
75 80 85	

ttt aag gct agg ttt ttt ggc gcg ttt tat aac gct gtg tta gga tca 342  
 Phe Lys Ala Arg Phe Phe Gly Ala Phe Tyr Asn Ala Val Leu Gly Ser  
 90 95 100  
 agg cta agg gat ttt tat gtg atg ctt tta acg ata ccc ttt att gcc 390  
 Arg Leu Arg Asp Phe Tyr Val Met Leu Leu Thr Ile Pro Phe Ile Ala  
 105 110 115 120  
 gct atc cat gag gtt tcg gcg tat tac ggg cat cct agc aac ttc ctt 438  
 Ala Ile His Glu Val Ser Ala Tyr Tyr Gly His Pro Ser Asn Phe Leu  
 125 130 135  
 ata gag ggt ttg gtc att ctt ggc ctt gtg tgt gtt ttt ggg att tgt 486  
 Ile Glu Gly Leu Val Ile Leu Gly Leu Val Cys Val Phe Gly Ile Cys  
 140 145 150  
 tct agg ctt tgc gct aaa tta ggg tgg tgatttaact caaatagcat 533  
 Ser Arg Leu Cys Ala Lys Leu Gly Trp  
 155 160  
 taaatggagg ggggagtaaa aaatta 559

<210> 174  
 <211> 161  
 <212> PRT  
 <213> Helicobacter pylori

<400> 174  
 Met Asn Val Lys Asn Arg Leu Ser Asp Trp Glu Tyr Gln Trp Ala Val  
 1 5 10 15  
 Ala Leu Val Tyr Thr Ile Cys Ile Ser Ile Asn Ala Arg Ile Phe Tyr  
 20 25 30  
 Asp Ile Asp Gly Ser Ala Ser Asp Ser Ile Phe Asp Pro Lys Asn Ser  
 35 40 45  
 Tyr Tyr Met Trp Leu Val Gly Leu Ile Ala Ala Leu Leu Ser Asn Leu  
 50 55 60  
 Leu Phe Asp Pro Arg Gly Arg Asp Cys Tyr Lys Ser Phe Gln Val Arg  
 65 70 75 80  
 Tyr Pro Arg Phe Leu Lys Ala Ile Phe Lys Ala Arg Phe Phe Gly Ala  
 85 90 95  
 Phe Tyr Asn Ala Val Leu Gly Ser Arg Leu Arg Asp Phe Tyr Val Met  
 100 105 110  
 Leu Leu Thr Ile Pro Phe Ile Ala Ala Ile His Glu Val Ser Ala Tyr  
 115 120 125  
 Tyr Gly His Pro Ser Asn Phe Leu Ile Glu Gly Leu Val Ile Leu Gly  
 130 135 140  
 Leu Val Cys Val Phe Gly Ile Cys Ser Arg Leu Cys Ala Lys Leu Gly  
 145 150 155 160  
 Trp

<210> 175  
 <211> 810  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS

<222> (53)...(712)

<400> 175

tgagatcaaa cccgtagaac ttgtcaaggt aattcttgcg taaggaaata gc atg tta	58
Met Leu	
1	
ata acc acc caa cta tcc aaa cga ttt tac gcc aca ctc gct ctt tct	106
Ile Thr Thr Gln Leu Ser Lys Arg Phe Tyr Ala Thr Leu Ala Leu Ser	
5 10 15	
tgc gtg ttt tta acc atc act aac att ctt gtc aaa ggc tcg ttt atc	154
Cys Val Phe Leu Thr Ile Thr Asn Ile Leu Val Lys Gly Ser Phe Ile	
20 25 30	
aat ctt tta gca ggg ctt agt ggg gtt ttg tat gcg ttt ttt gcc gga	202
Asn Leu Leu Ala Gly Leu Ser Gly Val Leu Tyr Ala Phe Phe Ala Gly	
35 40 45 50	
gaa agg caa acg att tgc ttt gtg ttt ggt ctt gtt tat aat ttg agt	250
Glu Arg Gln Thr Ile Cys Phe Val Phe Gly Leu Val Tyr Asn Leu Ser	
55 60 65	
tac gct tat gtc gct tat cag tgg aaa tta aac gct gat gtg att tta	298
Tyr Ala Tyr Val Ala Tyr Gln Trp Lys Leu Asn Ala Asp Val Ile Leu	
70 75 80	
tgc ctt ttt ttg tat atg cca gta acg att tat ggg ctg ttc gca tgg	346
Cys Leu Phe Leu Tyr Met Pro Val Thr Ile Tyr Gly Leu Phe Ala Trp	
85 90 95	
aaa aag aca gag cag cat gaa ggc gtt atc aag gct caa aaa ctt tcc	394
Lys Lys Thr Glu Gln His Glu Gly Val Ile Lys Ala Gln Lys Leu Ser	
100 105 110	
aaa aat tgg cgt ttt ata ctc att tta ggc gta ggg gtt tta act tgt	442
Lys Asn Trp Arg Phe Ile Leu Ile Leu Gly Val Gly Val Leu Thr Cys	
115 120 125 130	
gtg agc gct ttg ttt ttt aaa gag att aaa acg aat ttt tta tgg gca	490
Val Ser Ala Leu Phe Phe Lys Glu Ile Lys Thr Asn Phe Leu Trp Ala	
135 140 145	
gag agt ttt aat ttc gtc atc ttt att att gct ttt att tta cag gtt	538
Glu Ser Phe Asn Phe Val Ile Phe Ile Ile Ala Phe Ile Leu Gln Val	
150 155 160	
ttg cgc tat ata gaa aat tat gcg cta gta act ttg ggg aat atc gta	586
Leu Arg Tyr Ile Glu Asn Tyr Ala Leu Val Thr Leu Gly Asn Ile Val	
165 170 175	
tcc att atc gtg tgg ttt tgt att ttt caa att tct aca gag agc ttg	634
Ser Ile Ile Val Trp Phe Cys Ile Phe Gln Ile Ser Thr Glu Ser Leu	
180 185 190	
gtg caa ctc ttc aca acg atc cta tac ctt ttt att ggc ttg tat tat	682
Val Gln Leu Phe Thr Thr Ile Leu Tyr Leu Phe Ile Gly Leu Tyr Tyr	
195 200 205 210	

ttt aac cgg tgg aat aag tca tgc aag cag tgattttagc gaatggggag 732  
Phe Asn Arg Trp Asn Lys Ser Cys Lys Gln  
215 220

tttcctaaat ctcaaaaatg cttagacctt ttaaaaaacg cttcccttttt aatcgcatgc 792  
gatggggctg ttacctca 810

<210> 176  
<211> 220  
<212> PRT  
<213> Helicobacter pylori

<400> 176  
Met Leu Ile Thr Thr Gln Leu Ser Lys Arg Phe Tyr Ala Thr Leu Ala  
1 5 10 15  
Leu Ser Cys Val Phe Leu Thr Ile Thr Asn Ile Leu Val Lys Gly Ser  
20 25 30  
Phe Ile Asn Leu Leu Ala Gly Leu Ser Gly Val Leu Tyr Ala Phe Phe  
35 40 45  
Ala Gly Glu Arg Gln Thr Ile Cys Phe Val Phe Gly Leu Val Tyr Asn  
50 55 60  
Leu Ser Tyr Ala Tyr Val Ala Tyr Gln Trp Lys Leu Asn Ala Asp Val  
65 70 75 80  
Ile Leu Cys Leu Phe Leu Tyr Met Pro Val Thr Ile Tyr Gly Leu Phe  
85 90 95  
Ala Trp Lys Lys Thr Glu Gln His Glu Gly Val Ile Lys Ala Gln Lys  
100 105 110  
Leu Ser Lys Asn Trp Arg Phe Ile Leu Ile Leu Gly Val Gly Val Leu  
115 120 125  
Thr Cys Val Ser Ala Leu Phe Phe Lys Glu Ile Lys Thr Asn Phe Leu  
130 135 140  
Trp Ala Glu Ser Phe Asn Phe Val Ile Phe Ile Ile Ala Phe Ile Leu  
145 150 155 160  
Gln Val Leu Arg Tyr Ile Glu Asn Tyr Ala Leu Val Thr Leu Gly Asn  
165 170 175  
Ile Val Ser Ile Ile Val Trp Phe Cys Ile Phe Gln Ile Ser Thr Glu  
180 185 190  
Ser Leu Val Gln Leu Phe Thr Thr Ile Leu Tyr Leu Phe Ile Gly Leu  
195 200 205  
Tyr Tyr Phe Asn Arg Trp Asn Lys Ser Cys Lys Gln  
210 215 220

<210> 177  
<211> 451  
<212> DNA  
<213> Helicobacter pylori

<220>  
<221> CDS  
<222> (51)...(398)

<400> 177  
agtttaaaga aaagattaga aaaattagaa gataaaggag gtaacgactg atg aga 56  
Met Arg  
1

cac aaa cac gga tac cgc aag ctt ggg aga acc agc tcg cac aga aag 104  
His Lys His Gly Tyr Arg Lys Leu Gly Arg Thr Ser Ser His Arg Lys  
5 10 15

gcg tta tta aag aat tta gcg atc gct ttg att gag cat aac aaa att 152  
Ala Leu Leu Lys Asn Leu Ala Ile Ala Leu Ile Glu His Asn Lys Ile  
20 25 30

gaa aca ggg att tat aag gct aag gaa ttg cgc agt tac att gag aaa 200  
Glu Thr Gly Ile Tyr Lys Ala Lys Glu Leu Arg Ser Tyr Ile Glu Lys  
35 40 45 50

ttg acg aca gcg gct cgt gtg ggc gat ttt aat gcg cac cgc cat gtt 248  
Leu Thr Thr Ala Ala Arg Val Gly Asp Phe Asn Ala His Arg His Val  
55 60 65

ttt gca tat ttg caa aac aaa gaa gcc acc cac aag ctt gta act gaa 296  
Phe Ala Tyr Leu Gln Asn Lys Glu Ala Thr His Lys Leu Val Thr Glu  
70 75 80

atc gcg ccc aaa tac gcg caa agg aat ggc gga tac acc agg atc caa 344  
Ile Ala Pro Lys Tyr Ala Gln Arg Asn Gly Gly Tyr Thr Arg Ile Gln  
85 90 95

cgc acc act ttt aga aga ggg gac gct tcc act cta gcc acc att gaa 392  
Arg Thr Thr Phe Arg Arg Gly Asp Ala Ser Thr Leu Ala Thr Ile Glu  
100 105 110

ttt gta tgaaatttga tgaactgcta gccaaagattt agtcttggtt ggtggttattc 448  
Phe Val  
115

gct 451

<210> 178  
<211> 116  
<212> PRT  
<213> Helicobacter pylori

<400> 178  
Met Arg His Lys His Gly Tyr Arg Lys Leu Gly Arg Thr Ser Ser His  
1 5 10 15  
Arg Lys Ala Leu Lys Asn Leu Ala Ile Ala Leu Ile Glu His Asn  
20 25 30  
Lys Ile Glu Thr Gly Ile Tyr Lys Ala Lys Glu Leu Arg Ser Tyr Ile  
35 40 45  
Glu Lys Leu Thr Thr Ala Ala Arg Val Gly Asp Phe Asn Ala His Arg  
50 55 60  
His Val Phe Ala Tyr Leu Gln Asn Lys Glu Ala Thr His Lys Leu Val  
65 70 75 80  
Thr Glu Ile Ala Pro Lys Tyr Ala Gln Arg Asn Gly Gly Tyr Thr Arg  
85 90 95  
Ile Gln Arg Thr Thr Phe Arg Arg Gly Asp Ala Ser Thr Leu Ala Thr  
100 105 110  
Ile Glu Phe Val  
115

<210> 179  
<211> 1204  
<212> DNA  
<213> Helicobacter pylori

**06063**

-202-



09895913 "062901

65					70					75					80
Gly	Asp	Phe	Ser	Asp	Phe	Phe	Glu	Asp	Leu	Gly	Ser	Phe	Phe	Glu	Asp
				85					90					95	
Ala	Phe	Gly	Phe	Gly	Ala	Arg	Gly	Ser	Lys	Arg	Gln	Lys	Ser	Ser	Ile
			100					105					110		
Ala	Pro	Asp	Tyr	Leu	Gln	Thr	Leu	Glu	Leu	Ser	Phe	Lys	Glu	Ala	Val
		115					120					125			
Phe	Gly	Cys	Lys	Lys	Thr	Ile	Lys	Val	Gln	Tyr	Gln	Ser	Val	Cys	Glu
	130					135					140				
Ser	Cys	Asp	Gly	Thr	Gly	Ala	Lys	Asp	Lys	Ala	Leu	Glu	Thr	Cys	Lys
145					150					155					160
Gln	Cys	Asn	Gly	Gln	Gly	Gln	Val	Phe	Met	Arg	Gln	Gly	Phe	Met	Ser
			165					170						175	
Phe	Ala	Gln	Thr	Cys	Gly	Ala	Cys	Gln	Gly	Lys	Gly	Lys	Ile	Val	Lys
			180					185					190		
Thr	Pro	Cys	Gln	Ala	Cys	Lys	Gly	Lys	Thr	Tyr	Ile	Leu	Lys	Asp	Glu
		195					200					205			
Glu	Ile	Asp	Ala	Ile	Ile	Pro	Glu	Gly	Ile	Asp	Asp	Gln	Asn	Arg	Met
	210					215					220				
Val	Leu	Lys	Asn	Lys	Gly	Asn	Glu	Tyr	Glu	Lys	Gly	Lys	Arg	Gly	Asp
225					230					235					240
Leu	Tyr	Leu	Glu	Ala	Gln	Val	Lys	Glu	Asp	Glu	His	Phe	Lys	Arg	Glu
			245					250					255		
Gly	Cys	Asp	Leu	Phe	Ile	Lys	Ala	Pro	Val	Phe	Phe	Thr	Thr	Ile	Ala
			260					265					270		
Leu	Gly	His	Thr	Ile	Lys	Val	Pro	Ser	Leu	Lys	Gly	Asp	Glu	Leu	Glu
		275					280					285			
Leu	Lys	Ile	Pro	Arg	Asn	Ala	Arg	Asp	Lys	Gln	Thr	Phe	Ala	Phe	Arg
	290					295					300				
Asn	Glu	Gly	Val	Lys	His	Pro	Glu	Ser	Ser	Tyr	Arg	Gly	Ser	Leu	Ile
305					310					315					320
Val	Glu	Leu	Gln	Val	Ile	Tyr	Pro	Lys	Ser	Leu	Asn	Lys	Glu	Gln	Gln
			325						330				335		
Glu	Leu	Leu	Glu	Lys	Leu	His	Ala	Ser	Phe	Gly	Tyr	Glu	Gly	Glu	Pro
			340					345					350		
His	Lys	Ser	Val	Leu	Glu	Thr	Cys	Ile	Ser	Lys	Ile	Lys	Asp	Trp	Phe
		355					360					365			
Lys															

<210> 181  
 <211> 810  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (12)...(779)

<400> 181	
cgcatggaga a atg agg gta atg gcc aaa att gaa ttg tta gcc aaa ttc	50
Met Arg Val Met Ala Lys Ile Glu Leu Leu Ala Lys Phe	
1 5 10	
acg caa atc gcg ctc cct aac agc cac cct tta ttg aaa aaa gtt tta	98
Thr Gln Ile Ala Leu Pro Asn Ser His Pro Leu Leu Lys Lys Val Leu	
15 20 25	
aac tac gcc aaa aag cat ttc agc cag tgc cac atg ctc tct tca tcg	146



Asn	Tyr	Ala	Lys	Lys	His	Phe	Ser	Gln	Cys	His	Met	Leu	Ser	Ser	Ser			
30					35					40							45	
tta	ctc	atc	tta	aac	gac	acg	gaa	tgc	ttt	aaa	aaa	aac	tac	ttg	ctt			194
Leu	Leu	Ile	Leu	Asn	Asp	Thr	Glu	Cys	Phe	Lys	Lys	Asn	Tyr	Leu	Leu			
				50					55					60				
aat	tgg	gtc	tat	cat	gcc	ctt	gaa	tgc	gtg	cat	gaa	aaa	gat	att	agc			242
Asn	Trp	Val	Tyr	His	Ala	Leu	Glu	Cys	Val	His	Glu	Lys	Asp	Ile	Ser			
			65					70					75					
gcg	cat	tct	tta	gaa	gag	gtt	tta	caa	aaa	agc	cac	ctg	ccc	ata	cgc			290
Ala	His	Ser	Leu	Glu	Glu	Val	Leu	Gln	Lys	Ser	His	Leu	Pro	Ile	Arg			
			80					85					90					
atc	aaa	atc	atg	gct	caa	aac	acg	ctt	tta	gaa	aag	ata	gaa	gtg	aaa			338
Ile	Lys	Ile	Met	Ala	Gln	Asn	Thr	Leu	Leu	Glu	Lys	Ile	Glu	Val	Lys			
	95					100					105							
gtt	tta	acc	ttt	ggg	gcg	gaa	tat	gcg	ctt	ttt	atc	acc	aaa	cac	cct			386
Val	Leu	Thr	Phe	Gly	Ala	Glu	Tyr	Ala	Leu	Phe	Ile	Thr	Lys	His	Pro			
110					115					120					125			
atc	gcc	aag	cgg	ttt	tta	cgc	caa	aaa	ttt	agc	ggc	tgt	gtg	ttt	tta			434
Ile	Ala	Lys	Arg	Phe	Leu	Arg	Gln	Lys	Phe	Ser	Gly	Cys	Val	Phe	Leu			
				130					135					140				
gaa	acc	caa	gat	gaa	ttg	cat	ata	aga	ggc	gat	tca	gag	cgt	ttt	tgg			482
Glu	Thr	Gln	Asp	Glu	Leu	His	Ile	Arg	Gly	Asp	Ser	Glu	Arg	Phe	Trp			
			145					150					155					
gaa	ctc	att	gta	acg	ctc	aat	gaa	aat	aga	atc	gtc	cat	aac	gca	tgc			530
Glu	Leu	Ile	Val	Thr	Leu	Asn	Glu	Asn	Arg	Ile	Val	His	Asn	Ala	Cys			
			160					165					170					
tta	gat	ttc	atc	tac	cct	aat	ggc	ttt	ggc	aag	gac	agc	tac	acc	act			578
Leu	Asp	Phe	Ile	Tyr	Pro	Asn	Gly	Phe	Gly	Lys	Asp	Ser	Tyr	Thr	Thr			
	175					180					185							
atg	gct	gaa	cgc	aaa	tta	aaa	gaa	tgc	tat	aaa	acg	cta	ggg	ttt	atc			626
Met	Ala	Glu	Arg	Lys	Leu	Lys	Glu	Cys	Tyr	Lys	Thr	Leu	Gly	Phe	Ile			
190					195					200				205				
aag	cat	gaa	gat	ttc	agc	gaa	gtc	aaa	aag	cgc	tat	tta	gaa	ttg	gct			674
Lys	His	Glu	Asp	Phe	Ser	Glu	Val	Lys	Lys	Arg	Tyr	Leu	Glu	Leu	Ala			
				210					215					220				
aaa	acc	tac	cac	cct	gat	tta	tgc	gat	ctc	aaa	gaa	aaa	aag	gct	ctt			722
Lys	Thr	Tyr	His	Pro	Asp	Leu	Cys	Asp	Leu	Lys	Glu	Lys	Lys	Ala	Leu			
			225					230					235					
tat	gcc	aaa	cgc	ttc	gct	atc	att	caa	gag	gcg	tat	cgc	cac	att	aaa			770
Tyr	Ala	Lys	Arg	Phe	Ala	Ile	Ile	Gln	Glu	Ala	Tyr	Arg	His	Ile	Lys			
			240				245					250						
aaa	cac	gcc	taa	accccta	aactagccct	aatcgcgcta	g											810
Lys	His	Ala																
			255															

<210> 182  
 <211> 256  
 <212> PRT  
 <213> Helicobacter pylori

<400> 182  
 Met Arg Val Met Ala Lys Ile Glu Leu Leu Ala Lys Phe Thr Gln Ile  
 1 5 10 15  
 Ala Leu Pro Asn Ser His Pro Leu Leu Lys Lys Val Leu Asn Tyr Ala  
 20 25 30  
 Lys Lys His Phe Ser Gln Cys His Met Leu Ser Ser Ser Leu Leu Ile  
 35 40 45  
 Leu Asn Asp Thr Glu Cys Phe Lys Lys Asn Tyr Leu Leu Asn Trp Val  
 50 55 60  
 Tyr His Ala Leu Glu Cys Val His Glu Lys Asp Ile Ser Ala His Ser  
 65 70 75 80  
 Leu Glu Glu Val Leu Gln Lys Ser His Leu Pro Ile Arg Ile Lys Ile  
 85 90 95  
 Met Ala Gln Asn Thr Leu Leu Glu Lys Ile Glu Val Lys Val Leu Thr  
 100 105 110  
 Phe Gly Ala Glu Tyr Ala Leu Phe Ile Thr Lys His Pro Ile Ala Lys  
 115 120 125  
 Arg Phe Leu Arg Gln Lys Phe Ser Gly Cys Val Phe Leu Glu Thr Gln  
 130 135 140  
 Asp Glu Leu His Ile Arg Gly Asp Ser Glu Arg Phe Trp Glu Leu Ile  
 145 150 155 160  
 Val Thr Leu Asn Glu Asn Arg Ile Val His Asn Ala Cys Leu Asp Phe  
 165 170 175  
 Ile Tyr Pro Asn Gly Phe Gly Lys Asp Ser Tyr Thr Thr Met Ala Glu  
 180 185 190  
 Arg Lys Leu Lys Glu Cys Tyr Lys Thr Leu Gly Phe Ile Lys His Glu  
 195 200 205  
 Asp Phe Ser Glu Val Lys Lys Arg Tyr Leu Glu Leu Ala Lys Thr Tyr  
 210 215 220  
 His Pro Asp Leu Cys Asp Leu Lys Glu Lys Lys Ala Leu Tyr Ala Lys  
 225 230 235 240  
 Arg Phe Ala Ile Ile Gln Glu Ala Tyr Arg His Ile Lys Lys His Ala  
 245 250 255

<210> 183  
 <211> 900  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (59)...(778)

<400> 183  
 catgatgatt attataaaat cctaacgccg catgaacaaa taggatgggt caaaaaag 58  
 atg aag tca aat aaa aag tcc aat cgt tta aga gcg att tat aga gct 106  
 Met Lys Ser Asn Lys Lys Ser Asn Arg Leu Arg Ala Ile Tyr Arg Ala  
 1 5 10 15  
 tta gtg atc gct ata gga cta gct gtt atc atc gtt ttc aat tac ttt 154  
 Leu Val Ile Ala Ile Gly Leu Ala Val Ile Ile Val Phe Asn Tyr Phe  
 20 25 30  
 aac cgc aaa aac aat aac gcc cgc tcc agc cgt agg gct tgt tcg tgc 202

Asn	Arg	Lys	Asn	Asn	Asn	Ala	Arg	Ser	Ser	Arg	Arg	Ala	Cys	Ser	Cys		
		35					40					45					
ttt	ttt	tcc	ctt	acc	ggg	gtt	aat	tta	gaa	aaa	ata	ggc	act	ttt	gat	250	
Phe	Phe	Ser	Leu	Thr	Gly	Val	Asn	Leu	Glu	Lys	Ile	Gly	Thr	Phe	Asp		
	50					55					60						
acg	gac	gct	aaa	ctc	att	gtc	tta	aac	cac	caa	agc	tta	cta	gac	atc	298	
Thr	Asp	Ala	Lys	Leu	Ile	Val	Leu	Asn	His	Gln	Ser	Leu	Leu	Asp	Ile		
65					70					75					80		
att	tat	tta	gaa	gcc	tac	cac	cct	aga	aat	att	tgc	tgg	atc	gct	aaa	346	
Ile	Tyr	Leu	Glu	Ala	Tyr	His	Pro	Arg	Asn	Ile	Cys	Trp	Ile	Ala	Lys		
				85					90					95			
aaa	gag	ctg	ggc	gaa	atc	cct	ttt	tat	ggg	cat	gcc	tta	acg	gat	acc	394	
Lys	Glu	Leu	Gly	Glu	Ile	Pro	Phe	Tyr	Gly	His	Ala	Leu	Thr	Asp	Thr		
			100					105					110				
gga	atg	att	tta	att	gac	aga	gag	gat	aaa	aag	ggg	att	gtg	agc	ctt	442	
Gly	Met	Ile	Leu	Ile	Asp	Arg	Glu	Asp	Lys	Lys	Gly	Ile	Val	Ser	Leu		
		115						120					125				
ttg	aaa	gcg	tgt	aaa	gaa	aaa	tta	gac	caa	aac	cgc	cct	tta	gtg	att	490	
Leu	Lys	Ala	Cys	Lys	Glu	Lys	Leu	Asp	Gln	Asn	Arg	Pro	Leu	Val	Ile		
	130					135					140						
ttc	cct	gaa	ggc	act	aga	ggc	aaa	gga	gga	gaa	aaa	ttc	ctc	cct	ttc	538	
Phe	Pro	Glu	Gly	Thr	Arg	Gly	Lys	Gly	Gly	Glu	Lys	Phe	Leu	Pro	Phe		
145					150					155					160		
aag	caa	ggg	gct	aaa	atc	atc	gcc	gaa	aaa	ttc	cag	ctc	aaa	atc	caa	586	
Lys	Gln	Gly	Ala	Lys	Ile	Ile	Ala	Glu	Lys	Phe	Gln	Leu	Lys	Ile	Gln		
				165					170					175			
ccc	atg	gtg	tta	atc	aat	tcc	att	aaa	atc	ttt	aat	tcc	aag	cct	cta	634	
Pro	Met	Val	Leu	Ile	Asn	Ser	Ile	Lys	Ile	Phe	Asn	Ser	Lys	Pro	Leu		
			180					185					190				
gaa	gcc	tat	aaa	gcg	cgc	acc	cgt	tta	gtc	atg	cta	gaa	agc	tat	acg	682	
Glu	Ala	Tyr	Lys	Ala	Arg	Thr	Arg	Leu	Val	Met	Leu	Glu	Ser	Tyr	Thr		
		195					200					205					
cct	gat	ttt	aac	tcg	ccc	acc	tgg	tat	gaa	gaa	tta	caa	gaa	cgc	atg	730	
Pro	Asp	Phe	Asn	Ser	Pro	Thr	Trp	Tyr	Glu	Glu	Leu	Gln	Glu	Arg	Met		
	210					215					220						
caa	aaa	gag	tat	tta	aaa	cac	tat	cat	gaa	tta	aac	cct	agc	gaa	caa	778	
Gln	Lys	Glu	Tyr	Leu	Lys	His	Tyr	His	Glu	Leu	Asn	Pro	Ser	Glu	Gln		
225					230					235					240		
tgaagctttt	tgactacgct	cctttgagtt	tggcttggcg	ggagttttttg	caaagcgaat	838											
ttaaaaagcc	ttatttttta	gaaatagaaa	aacgctacct	agaagcccta	aaaatcccta	898											
aa						900											

<210> 184  
 <211> 240  
 <212> PRT  
 <213> Helicobacter pylori



Glu 55	Met	Thr	Gly	Ile	Glu	Cys 60	Val	Gln	Thr	Ile	Lys 65	Asp	Lys	Glu	Arg	
ttc	aag	cct	aaa	gac	gct	tta	atg	gaa	att	agg	ggg	gat	ttt	agc	atg	294
Phe 70	Lys	Pro	Lys	Asp	Ala	Leu	Met	Glu	Ile	Arg	Gly	Asp	Phe	Ser	Met 85	
ctt	tta	aag	gtt	gag	cgc	acc	ctt	tta	aac	ctt	ttg	caa	cac	agc	agc	342
Leu	Leu	Lys	Val	Glu	Arg	Thr	Leu	Leu	Asn	Leu	Leu	Gln	His	Ser	Ser	
				90					95					100		
ggg	att	gct	act	tta	acg	agc	cgt	ttt	gta	gag	gct	tta	aat	tct	cat	390
Gly	Ile	Ala	Thr	Leu	Thr	Ser	Arg	Phe	Val	Glu	Ala	Leu	Asn	Ser	His	
			105					110					115			
aaa	gtg	cgt	ttg	ttg	gac	acg	aga	aaa	acg	aga	ccc	ctt	tta	agg	atc	438
Lys	Val	Arg	Leu	Leu	Asp	Thr	Arg	Lys	Thr	Arg	Pro	Leu	Leu	Arg	Ile	
		120					125					130				
ttt	gaa	aaa	tat	tcc	gtg	ctt	aat	ggg	gga	gcg	agc	aac	cac	cgc	tta	486
Phe	Glu	Lys	Tyr	Ser	Val	Leu	Asn	Gly	Gly	Ala	Ser	Asn	His	Arg	Leu	
	135					140					145					
ggg	cta	gat	gac	gct	tta	atg	ctt	aaa	gac	acg	cat	tta	agg	cat	gtg	534
Gly	Leu	Asp	Asp	Ala	Leu	Met	Leu	Lys	Asp	Thr	His	Leu	Arg	His	Val	
150				155					160						165	
aaa	gat	ctc	aaa	agc	ttt	tta	acg	cat	gcc	aga	aaa	aac	ttg	cct	ttc	582
Lys	Asp	Leu	Lys	Ser	Phe	Leu	Thr	His	Ala	Arg	Lys	Asn	Leu	Pro	Phe	
				170					175					180		
acg	gct	aaa	att	gaa	att	gaa	tgc	gaa	agc	ttt	gaa	gag	gcc	aaa	aac	630
Thr	Ala	Lys	Ile	Glu	Ile	Glu	Cys	Glu	Ser	Phe	Glu	Glu	Ala	Lys	Asn	
			185				190					195				
gcc	atg	aat	gcg	gga	gcg	gat	att	gtg	atg	tgc	gat	aat	ttg	agc	gtt	678
Ala	Met	Asn	Ala	Gly	Ala	Asp	Ile	Val	Met	Cys	Asp	Asn	Leu	Ser	Val	
		200					205					210				
tta	gag	act	aaa	gaa	att	gcc	gct	tat	aga	gat	gcg	cat	tat	ccc	ttt	726
Leu	Glu	Thr	Lys	Glu	Ile	Ala	Ala	Tyr	Arg	Asp	Ala	His	Tyr	Pro	Phe	
	215					220					225					
gtt	tta	ctg	gaa	gcg	agc	ggg	aac	att	tca	cta	gag	agc	att	aac	gct	774
Val	Leu	Leu	Glu	Ala	Ser	Gly	Asn	Ile	Ser	Leu	Glu	Ser	Ile	Asn	Ala	
230				235						240					245	
tac	gct	aaa	agc	ggc	gtg	gat	gcc	att	agc	gta	ggg	gct	tta	atc	cat	822
Tyr	Ala	Lys	Ser	Gly	Val	Asp	Ala	Ile	Ser	Val	Gly	Ala	Leu	Ile	His	
			250						255				260			
caa	gcc	act	ttt	att	gac	atg	cac	atg	aaa	atg	gct	taaagacttt				868
Gln	Ala	Thr	Phe	Ile	Asp	Met	His	Met	Lys	Met	Ala					
			265					270								

<210> 186  
 <211> 273  
 <212> PRT  
 <213> Helicobacter pylori

<400> 186  
 Met Glu Ile Arg Thr Phe Leu Glu Arg Ala Leu Lys Glu Asp Leu Gly  
 1 5 10 15  
 His Gly Asp Leu Phe Glu Arg Val Leu Glu Lys Asp Phe Lys Ala Thr  
 20 25 30  
 Ala Phe Val Arg Ala Lys Gln Glu Gly Val Phe Ser Gly Glu Lys Tyr  
 35 40 45  
 Ala Leu Glu Leu Leu Glu Met Thr Gly Ile Glu Cys Val Gln Thr Ile  
 50 55 60  
 Lys Asp Lys Glu Arg Phe Lys Pro Lys Asp Ala Leu Met Glu Ile Arg  
 65 70 75 80  
 Gly Asp Phe Ser Met Leu Leu Lys Val Glu Arg Thr Leu Leu Asn Leu  
 85 90 95  
 Leu Gln His Ser Ser Gly Ile Ala Thr Leu Thr Ser Arg Phe Val Glu  
 100 105 110  
 Ala Leu Asn Ser His Lys Val Arg Leu Leu Asp Thr Arg Lys Thr Arg  
 115 120 125  
 Pro Leu Leu Arg Ile Phe Glu Lys Tyr Ser Val Leu Asn Gly Gly Ala  
 130 135 140  
 Ser Asn His Arg Leu Gly Leu Asp Asp Ala Leu Met Leu Lys Asp Thr  
 145 150 155 160  
 His Leu Arg His Val Lys Asp Leu Lys Ser Phe Leu Thr His Ala Arg  
 165 170 175  
 Lys Asn Leu Pro Phe Thr Ala Lys Ile Glu Ile Glu Cys Glu Ser Phe  
 180 185 190  
 Glu Glu Ala Lys Asn Ala Met Asn Ala Gly Ala Asp Ile Val Met Cys  
 195 200 205  
 Asp Asn Leu Ser Val Leu Glu Thr Lys Glu Ile Ala Ala Tyr Arg Asp  
 210 215 220  
 Ala His Tyr Pro Phe Val Leu Leu Glu Ala Ser Gly Asn Ile Ser Leu  
 225 230 235 240  
 Glu Ser Ile Asn Ala Tyr Ala Lys Ser Gly Val Asp Ala Ile Ser Val  
 245 250 255  
 Gly Ala Leu Ile His Gln Ala Thr Phe Ile Asp Met His Met Lys Met  
 260 265 270  
 Ala

<210> 187  
 <211> 1153  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (51)...(1100)

<400> 187  
 gatcaaacgc tacaacccta gctgtctttt agaagtggat gggggcgtga atg ata 56  
 Met Ile  
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aaa ata tct ttg aac tcc aac aag cgg gcg tgg atg tgg tgg ttt cag 104  
 Lys Ile Ser Leu Asn Ser Asn Lys Arg Ala Trp Met Trp Trp Phe Gln

05895913-062901

5	10	15	
gga gtt ata ttt tta aat cca aag atc gta agc tgg cta ttg aag gct Gly Val Ile Phe Leu Asn Pro Lys Ile Val Ser Trp Leu Leu Lys Ala 20 25 30			152
tac aga atg tca gac aat ctc ttg cat aaa gac atc caa gcc cta atc Tyr Arg Met Ser Asp Asn Leu Leu His Lys Asp Ile Gln Ala Leu Ile 35 40 45 50			200
gct cgc tta aag cgc cag gac tta agc ttg ggc atg cta gaa aaa tcg Ala Arg Leu Lys Arg Gln Asp Leu Ser Leu Gly Met Leu Glu Lys Ser 55 60 65			248
ctc tct cgc ctt att cat gat gaa atc aat ttg gag tat ttg aag gcg Leu Ser Arg Leu Ile His Asp Glu Ile Asn Leu Glu Tyr Leu Lys Ala 70 75 80			296
tgc ggg ctc aat ttc ata gaa acg agc gaa aat tta atc acg ctc aaa Cys Gly Leu Asn Phe Ile Glu Thr Ser Glu Asn Leu Ile Thr Leu Lys 85 90 95			344
aac ctt aaa acc ccc ctt aaa gat gag gtt ttt tcc ttt att gat tta Asn Leu Lys Thr Pro Leu Lys Asp Glu Val Phe Ser Phe Ile Asp Leu 100 105 110			392
gaa acc acc gga tct tgc ccc ata aag cat gag att tta gaa att ggg Glu Thr Thr Gly Ser Cys Pro Ile Lys His Glu Ile Leu Glu Ile Gly 115 120 125 130			440
gcc gtg caa gtg aaa ggg ggg gaa att atc aat cgt ttt gaa acc ctt Ala Val Gln Val Lys Gly Gly Glu Ile Ile Asn Arg Phe Glu Thr Leu 135 140 145			488
gtg aaa gtc aaa agc gtg cct gat tat atc gct gag ctt aca ggc atc Val Lys Val Lys Ser Val Pro Asp Tyr Ile Ala Glu Leu Thr Gly Ile 150 155 160			536
act tat gaa gac acc cta aac gcc cca agc gcg cat gaa gct ttg caa Thr Tyr Glu Asp Thr Leu Asn Ala Pro Ser Ala His Glu Ala Leu Gln 165 170 175			584
gaa ttg cgg ctt ttt tta ggc aat agc gtg ttt gtg gcc cac aac gct Glu Leu Arg Leu Phe Leu Gly Asn Ser Val Phe Val Ala His Asn Ala 180 185 190			632
aat ttt gat tac aac ttt ttg ggg cgt tat ttt gta gaa aaa ttg cat Asn Phe Asp Tyr Asn Phe Leu Gly Arg Tyr Phe Val Glu Lys Leu His 195 200 205 210			680
tgc cct tta ttg aat tta aag ctt tgc act ctg gat tta tcc aaa cga Cys Pro Leu Leu Asn Leu Lys Leu Cys Thr Leu Asp Leu Ser Lys Arg 215 220 225			728
gcc att ttg tcc atg cgt tat tct ttg agc ttt tta aaa gag ctt tta Ala Ile Leu Ser Met Arg Tyr Ser Leu Ser Phe Leu Lys Glu Leu Leu 230 235 240			776
ggg ttt ggt ata gaa gtc agc cat aga gcc tat gcg gac gct tta gcg			824





Asn Ala Asn Phe Asp Tyr Asn Phe Leu Gly Arg Tyr Phe Val Glu Lys  
 195 200 205  
 Leu His Cys Pro Leu Leu Asn Leu Lys Leu Cys Thr Leu Asp Leu Ser  
 210 215 220  
 Lys Arg Ala Ile Leu Ser Met Arg Tyr Ser Leu Ser Phe Leu Lys Glu  
 225 230 235 240  
 Leu Leu Gly Phe Gly Ile Glu Val Ser His Arg Ala Tyr Ala Asp Ala  
 245 250 255  
 Leu Ala Ser Tyr Lys Leu Phe Glu Ile Cys Leu Leu Asn Leu Pro Ser  
 260 265 270  
 Tyr Ile Lys Thr Thr Met Asp Leu Ile Asp Phe Ser Lys Cys Ala Asn  
 275 280 285  
 Thr Leu Ile Lys Arg Pro Pro Lys Ala Arg Tyr Gln Glu Ile Pro Ser  
 290 295 300  
 Pro Phe Ser Leu Phe Glu Lys Thr Lys Gly Leu Phe Asn His Lys Ser  
 305 310 315 320  
 Asn Gln Leu Asn Glu Ser Cys Leu Met Gly Phe Met Gly Thr Glu Ile  
 325 330 335  
 Leu Ala Ser Leu Phe Asp Thr Phe Glu Cys Cys Leu Val Phe  
 340 345 350

<210> 189  
 <211> 990  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (52)...(864)

<400> 189  
 aaaaacactt tttaatgtta taatctatcc taaacaatat aagggggtttt t atg gca 57  
 Met Ala  
 1  
 aaa att gaa agc aat gat tcc cac cta aga ggt att tta aaa gac gaa 105  
 Lys Ile Glu Ser Asn Asp Ser His Leu Arg Gly Ile Leu Lys Asp Glu  
 5 10 15  
 ctc tac tat caa atc ccc atc tac caa cgc cct tat caa tgg aca gaa 153  
 Leu Tyr Tyr Gln Ile Pro Ile Tyr Gln Arg Pro Tyr Gln Trp Thr Glu  
 20 25 30  
 gaa aac tgc gaa aaa ctt tta gac gat ttg ttt ttt aat tat gaa gat 201  
 Glu Asn Cys Glu Lys Leu Leu Asp Asp Leu Phe Phe Asn Tyr Glu Asp  
 35 40 45 50  
 gac aga gaa ggc gat tat ttt tgc ggc tca tta gtc tta att gca atc 249  
 Asp Arg Glu Gly Asp Tyr Phe Cys Gly Ser Leu Val Leu Ile Ala Ile  
 55 60 65  
 agc aaa gat tct aaa gcc aca acc tat gat gtt gta gat ggc cag caa 297  
 Ser Lys Asp Ser Lys Ala Thr Thr Tyr Asp Val Val Asp Gly Gln Gln  
 70 75 80  
 cgc tta agc act ttc att ctg ctt gca aaa gtt tta gcc gat ctt tat 345  
 Arg Leu Ser Thr Phe Ile Leu Leu Ala Lys Val Leu Ala Asp Leu Tyr  
 85 90 95

aat gat tgt tta gac cct aag aat tta gaa cat tta caa gag ggt tgg	393
Asn Asp Cys Leu Asp Pro Lys Asn Leu Glu His Leu Gln Glu Gly Trp	
100 105 110	
aaa gat agg cat aca gaa aga aaa cga ctg agt ttt aac act ata ggg	441
Lys Asp Arg His Thr Glu Arg Lys Arg Leu Ser Phe Asn Thr Ile Gly	
115 120 125 130	
tct aac gct gaa tat gat ttt caa gat gca tta gaa cat ttc aac gac	489
Ser Asn Ala Glu Tyr Asp Phe Gln Asp Ala Leu Glu His Phe Asn Asp	
135 140 145	
tct caa gca agc aag aat aaa aat aat aag aac aat tac cta aaa aat	537
Ser Gln Ala Ser Lys Asn Lys Asn Asn Lys Asn Asn Tyr Leu Lys Asn	
150 155 160	
gcg atc tgt tta aaa gac tat ctc atg aaa aaa gag att aaa aac att	585
Ala Ile Cys Leu Lys Asp Tyr Leu Met Lys Lys Glu Ile Lys Asn Ile	
165 170 175	
aac gat ttc att gag tgg ctg tat tct aat gtt aaa ttt atc acc atc	633
Asn Asp Phe Ile Glu Trp Leu Tyr Ser Asn Val Lys Phe Ile Thr Ile	
180 185 190	
att tgc cca aac ata gac aag gca tta agg att ttt aat gtt tta aac	681
Ile Cys Pro Asn Ile Asp Lys Ala Leu Arg Ile Phe Asn Val Leu Asn	
195 200 205 210	
gct agg ggt ttg cct ttg aat gcg aca gat att ttt aag ggg gaa tta	729
Ala Arg Gly Leu Pro Leu Asn Ala Thr Asp Ile Phe Lys Gly Glu Leu	
215 220 225	
tta aaa cac gct aaa gag cat gag cga gaa gaa ttt gtg tct cgt tgg	777
Leu Lys His Ala Lys Glu His Glu Arg Glu Glu Phe Val Ser Arg Trp	
230 235 240	
aac gcc tta agc caa aaa tgc tcg gac aat gat tta aca atg gag aca	825
Asn Ala Leu Ser Gln Lys Cys Ser Asp Asn Asp Leu Thr Met Glu Thr	
245 250 255	
tta ttc agt tgg tat aac cta tct caa tcc ggt aac ttc tagagacaaa	874
Leu Phe Ser Trp Tyr Asn Leu Ser Gln Ser Gly Asn Phe	
260 265 270	
atggaaaaag agctcggttac ttggttcaac atacttaaca aacccccctt agaatacctt	934
aagggcgtag aggattttta caacgcttat ggtgagggtg tagaaatgca agatcg	990

<210> 190

<211> 271

<212> PRT

<213> Helicobacter pylori

<400> 190

Met Ala Lys Ile Glu Ser Asn Asp Ser His Leu Arg Gly Ile Leu Lys	
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Asp Glu Leu Tyr Tyr Gln Ile Pro Ile Tyr Gln Arg Pro Tyr Gln Trp	
20 25 30	
Thr Glu Glu Asn Cys Glu Lys Leu Leu Asp Asp Leu Phe Phe Asn Tyr	
35 40 45	

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Glu Asp Asp Arg Glu Gly Asp Tyr Phe Cys Gly Ser Leu Val Leu Ile  
 50 55 60  
 Ala Ile Ser Lys Asp Ser Lys Ala Thr Thr Tyr Asp Val Val Asp Gly  
 65 70 75 80  
 Gln Gln Arg Leu Ser Thr Phe Ile Leu Leu Ala Lys Val Leu Ala Asp  
 85 90 95  
 Leu Tyr Asn Asp Cys Leu Asp Pro Lys Asn Leu Glu His Leu Gln Glu  
 100 105 110  
 Gly Trp Lys Asp Arg His Thr Glu Arg Lys Arg Leu Ser Phe Asn Thr  
 115 120 125  
 Ile Gly Ser Asn Ala Glu Tyr Asp Phe Gln Asp Ala Leu Glu His Phe  
 130 135 140  
 Asn Asp Ser Gln Ala Ser Lys Asn Lys Asn Asn Lys Asn Asn Tyr Leu  
 145 150 155 160  
 Lys Asn Ala Ile Cys Leu Lys Asp Tyr Leu Met Lys Lys Glu Ile Lys  
 165 170 175  
 Asn Ile Asn Asp Phe Ile Glu Trp Leu Tyr Ser Asn Val Lys Phe Ile  
 180 185 190  
 Thr Ile Ile Cys Pro Asn Ile Asp Lys Ala Leu Arg Ile Phe Asn Val  
 195 200 205  
 Leu Asn Ala Arg Gly Leu Pro Leu Asn Ala Thr Asp Ile Phe Lys Gly  
 210 215 220  
 Glu Leu Leu Lys His Ala Lys Glu His Glu Arg Glu Glu Phe Val Ser  
 225 230 235 240  
 Arg Trp Asn Ala Leu Ser Gln Lys Cys Ser Asp Asn Asp Leu Thr Met  
 245 250 255  
 Glu Thr Leu Phe Ser Trp Tyr Asn Leu Ser Gln Ser Gly Asn Phe  
 260 265 270

<210> 191  
 <211> 283  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (51)...(230)

<400> 191  
 ccctagaatg cgtgcttttg gctaaggaat ttttgcctaa cgctaggcctt atg gtg 56  
 Met Val  
 1  
 gct ggg ggg cgt gaa gtg gtg ttt aaa gat aat gac aaa aag gaa gcc 104  
 Ala Gly Gly Arg Glu Val Val Phe Lys Asp Asn Asp Lys Lys Glu Ala  
 5 10 15  
 aag ctt ttt gaa tac ggc atc aat gcg gtg gtg cta ggg gac tat ttg 152  
 Lys Leu Phe Glu Tyr Gly Ile Asn Ala Val Val Leu Gly Asp Tyr Leu  
 20 25 30  
 acc acc aaa ggc aaa gcc cct aaa aaa gat ata gaa aaa ctg ctc tct 200  
 Thr Thr Lys Gly Lys Ala Pro Lys Lys Asp Ile Glu Lys Leu Leu Ser  
 35 40 45 50  
 tat ggc ttg aca atg gcg aca agc tgt cat taatgagaga acttttttaaa 250  
 Tyr Gly Leu Thr Met Ala Thr Ser Cys His  
 55 60

283

<400> 193																56																	
cactt	g	t	t	t	t	g	a	g	t	g	c	c	t	a	t	aggcataaata	agtcct	g	t	t	t	t	t	a	a	a	t	g	g		Trp	Trp	
																10	15	1															
tat	gat	aac	a	at	gtc	aac	tta	cag	ctt	ttt	tat	gga	ttt	tta	cac	a	at								104								
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**06093**

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 Ala Gly Leu Gly Gly Glu Ser Val Thr Pro Asn Val Leu Lys Asp Phe  
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 Gly Leu Arg Met Gly Asp Lys His His Thr Leu Glu Leu Ser Thr Ser  
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 Val His Gly Asp Ala Pro Ser Cys Ser Leu Lys Lys Leu Lys Ser Cys  
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 Asp Asn Asn Gln Asn Asn Glu Asn His Glu Asn Ser Ser Glu Asn Ser  
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 Lys Ala Asp Glu Met Arg Ala Gly Ala Phe Glu Arg Phe Thr Asn Arg  
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 Lys Lys Arg Phe Arg Glu Asn Ala Gln Lys Asn Ala Glu Tyr Ser Asn  
 35 40 45 50

cat gaa gcg tct tcg cac cat aaa aaa gag cat cgc cct aac aaa aaa 250  
 His Glu Ala Ser Ser His His Lys Lys Glu His Arg Pro Asn Lys Lys  
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**SECRET**

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cgg gtc tat caa gcc ata caa tac ggc att aaa tac aac cgc aag atc Arg Val Tyr Gln Ala Ile Gln Tyr Gly Ile Lys Tyr Asn Arg Lys Ile 375 380 385	1210
gct gtg atc ggg cgc tct atg gaa aaa aac cta gac atc gct aga gaa Ala Val Ile Gly Arg Ser Met Glu Lys Asn Leu Asp Ile Ala Arg Glu 390 395 400	1258
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caa ggc gaa acc atg agc gcg ctt tat cgc atg gcg act gat gaa cac Gln Gly Glu Thr Met Ser Ala Leu Tyr Arg Met Ala Thr Asp Glu His 435 440 445 450	1402
cgt cat att tct atc aaa ccc aac gat tta gtc atc att tcc gct aaa Arg His Ile Ser Ile Lys Pro Asn Asp Leu Val Ile Ile Ser Ala Lys 455 460 465	1450
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Ile Leu His Val Asn Glu Arg Gly Thr Leu Gly Phe His Lys Glu Leu			



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Pro	Leu	Gly	Gly	Leu	Gly	Glu	Ile	Gly	Gly	Asn	Met	Met	Val	Ile	Glu
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acc Thr	caa Gln 150	agc Ser	caa Gln	gaa Glu	tgc Cys	aaa Lys 155	gaa Glu	ttt Phe	atc Ile	aaa Lys	aac Asn 160	cgt Arg	tta Leu	aat Asn	tct Ser	537
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Lys	Ala	Lys	Val	Ala	Arg	Asp	Asn	Leu	Ile	Cys	Glu	Lys	Tyr	Lys	Asn	
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Ile	Tyr	Lys	Glu	Leu	Asn	Gly	Val	Ile	Leu	Ala	Ser	Phe	Ser	Thr	Leu	
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Lys	Asn	Leu	Gln	Gly	Ser	Asn	Phe	Lys	Lys	Phe	Arg	Glu	Ile	Phe	Lys	
			485					490						495		
Ala	Lys	Phe	Leu	Glu	Gly	Phe	Met	Val	Pro	Ala	Asp	Thr	Phe	Asp	Asn	
		500						505					510			
Val	Arg	Gly	Gln	Phe	Pro	Ile	Gly	Phe	Leu	Val	Trp	Asp	Thr	Ser	Ser	
		515					520					525				
Ile	Leu	Pro	Lys	Glu	Asn	Pro	Leu	Asn	Leu	Gly	Gly	Asn	Ser	Lys	Glu	
	530					535					540					
Glu	Lys	Gln	Asn	Ser	Asn	Leu	Ile	Leu	Asp	Gln	Asp	Asn	Leu	Lys	Asp	
545					550					555					560	
Asn	Pro	Leu	Lys	Glu	Arg	Phe	Cys	Leu	Leu	Asp	Ile	Asn	Ala	Pro	Asn	
			565					570						575		
Arg	Lys	Met	Cys	Ser	Gln	Ser	Arg	Thr	Arg	Thr	Lys	Gly	Thr	Gln	Lys	
		580						585					590			
His	Ser	Thr	Ala	Ala	Pro	Phe	Glu	Thr	Pro	Leu	His	Thr	Val	Ser	Leu	
		595					600					605				
Glu	Ile	Phe	Asp	Ser	Phe	Gly	Gly	Phe	Leu	Gly	Ser	Lys	Lys	Ile	Tyr	
	610					615					620					
Thr	His	Thr	Ile	Asp	Lys	Met	Leu	Thr	Leu	Ala	Asp	Tyr	Leu	Gln	Lys	
625					630					635					640	
Phe	Gln	Pro	Thr	Lys	Arg	Asp	Thr	Ile	Phe	Gly	Tyr	Leu	Asp	Pro	Gly	
			645						650					655		
Arg	Asn	Ser	Phe	Gln	His	Gln	Asn	Leu	Ile	His	Ile	Ser	Ile	Ile	Asp	
			660					665					670			
Lys	Ser	Lys	Gln	Ser	His	Val	Lys	Tyr	Phe	Pro	Ile	Ile	Ala	Thr	Thr	
		675					680					685				
Ile	Leu	Leu	Val	Ser	Val	Phe	Phe	Ser	Ile	Arg	His	Cys	Ile	Lys	Ala	
	690					695					700					
Thr	Trp	Gln	Asn	Asp	Arg	Asp	Gln	Phe	Tyr	Ala	Pro	Tyr	Asp	Asp	Ala	
705					710					715					720	
Phe	Gln	Asp	Asp	Ser	Glu	Phe	Lys	Asn	Asn	Cys	Leu	Ile	Phe	Met	Leu	

				725						730					735				
Phe	His	Thr	Gln	Asn	Arg	Ile	Thr	Thr	Ala	Gln	Gly	Thr	Asn	His	Phe				
			740						745				750						
Ile	Pro	Phe	Ser	Glu	Thr	Glu	Val	Asn	Ala	Lys	Glu	Arg	Tyr	Ser	Ser				
		755						760				765							
His	Ala	Leu	Leu	Glu	Phe	Leu	Lys	Gly	Glu	Ile	Lys	Glu	Leu	Lys	Glu				
	770					775					780								
Asn	Asp	Ser	Leu	Phe	Leu	Ser	Ala	Lys	Lys	Glu	Asn	Lys	Pro	Leu	Lys				
785					790					795				800					
Phe	Ser	Pro	Ser	Ala	Ser	Lys	Val	Phe	Asp	Ala	Ser	Arg	Glu	Val	Tyr				
				805					810					815					
Arg	Tyr	Tyr	His	Thr	Gln	Asp	Phe	Thr	Asn	Arg	Pro	Tyr	Asn	Ala	Asn				
			820					825					830						
Ala	Ser	Leu	Tyr	Asp	Ile	Lys	Glu	Phe	Phe	Gln	Gly	Arg	Asn	Lys	Gln				
		835					840					845							
Gly	Lys	Leu	Asn	Leu	Pro	Ala	Lys	Ala	Lys	Asp	Glu	Tyr	Tyr	Lys	Gln				
	850					855				860									
Leu	Tyr	Ala	Asn	Leu	Gln	Asp	Ala	Leu	Lys	Asp	Leu	Ala	Lys	Glu	Ile				
865					870					875				880					
Gln	Pro	Lys	Val	Tyr	Glu	Tyr	Gly	Phe	Leu	Arg	Glu								
				885					890										

<210> 199  
 <211> 996  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (70)...(948)

<400> 199	
aaaagccacg caatcagcca caaacatcat cacacaagcc tttggctatc aattattaat	60
gagataaaag atg tta gaa ttt att tta aaa att caa gct aga gac tct aaa	111
Met Leu Glu Phe Ile Leu Lys Ile Gln Ala Arg Asp Ser Lys	
1 5 10	
ggc ttg gtg agc acg att agc acc act atc gct aac aag ggc tat aac	159
Gly Leu Val Ser Thr Ile Ser Thr Thr Ile Ala Asn Lys Gly Tyr Asn	
15 20 25 30	
atc gtc aaa aac gat gaa ttt gtt gat ccc tta aaa cag cgt ttt ttc	207
Ile Val Lys Asn Asp Glu Phe Val Asp Pro Leu Lys Gln Arg Phe Phe	
35 40 45	
atg cgg tta aaa atc caa aaa gaa atc aag ccc ttg aat act gaa att	255
Met Arg Leu Lys Ile Gln Lys Glu Ile Lys Pro Leu Asn Thr Glu Ile	
50 55 60	
aaa gag caa gaa gag caa tcc tta aag acc gct ctt ttt aaa gcc cta	303
Lys Glu Gln Glu Glu Gln Ser Leu Lys Thr Ala Leu Phe Lys Ala Leu	
65 70 75	
gaa aac ttt aac gag tta ttg att gaa gtc att tta acg cat aaa aaa	351
Glu Asn Phe Asn Glu Leu Leu Ile Glu Val Ile Leu Thr His Lys Lys	
80 85 90	
aac atc att ctg ctc gct act aaa gag agc cat tgc tta ggg gat ttg	399
Asn Ile Ile Leu Leu Ala Thr Lys Glu Ser His Cys Leu Gly Asp Leu	



95	100	105	110	
ctt tta agg gtg tat ggg ggg gaa ttg aac gct caa att tta ggc gtt				447
Leu Leu Arg Val Tyr 115	Gly Gly Glu Leu 120	Asn Ala Gln Ile Leu 125	Gly Val	
att tcc aac cac gag att tta cgc cct tta gtg gaa aaa ttt gac atc				495
Ile Ser Asn His 130	Glu Ile Leu Arg Pro Leu Val Glu Lys 135	Phe Asp Ile 140		
cct tat ttt tat gcg cct tgc gac aat caa gtt ttg cat gaa aaa gaa				543
Pro Tyr Phe Tyr 145	Ala Pro Cys Asp Asn Gln Val Leu His 150	Glu Lys Glu 155		
gtt tta gaa atc att aaa aac ctg gaa tta aag cac aaa gtg agt gca				591
Val Leu Glu Ile Ile Lys 160	Asn Leu Glu Leu Lys 165	His Lys Val Ser Ala 170		
gac ttg ctc gtt tta gcc aaa tac atg cgc att tta agc cat gat ttt				639
Asp Leu Leu Val Leu 175	Ala Lys Tyr Met Arg Ile Leu Ser His 180	Asp Phe 185		
acg aag cgc tat gaa aac cag atc tta aat atc cat cat agt ttc ttg				687
Thr Lys Arg Tyr 195	Glu Asn Gln Ile Leu Asn Ile His His 200	Ser Phe Leu 205		
ccc gca ttc att ggg gct aat cct tac cag caa gcg ttt gaa agg ggc				735
Pro Ala Phe Ile 210	Gly Ala Asn Pro Tyr Gln Gln Ala Phe 215	Glu Arg Gly 220		
gtg aaa gtc atc ggg gcc acg gcg cat ttt gtg aat gaa agc ctt gat				783
Val Lys Val Ile Gly 225	Ala Thr Ala His Phe Val Asn Glu Ser Leu 230	Asp 235		
gct ggg ccg att atc ata caa gac act ctg ccc att aac cac aat tac				831
Ala Gly Pro Ile Ile Ile 240	Gln Asp Thr Leu Pro Ile 245	Asn His Asn Tyr 250		
agc gtg gaa aaa atg cgc cta gcg ggt aag gat ata gaa aaa ctg gtt				879
Ser Val Glu Lys Met 255	Arg Leu Ala Gly Lys Asp 260	Ile Glu Lys Leu Val 265		
tta gct agg gct tta aaa ctc gtt tta gaa gac aga gtc ttt gta cat				927
Leu Ala Arg Ala Leu Lys 275	Leu Val Leu Glu Asp Arg Val Phe 280	Val His 285		
gaa aat aaa acg gtg gtg ttt tgaatgcttt tagatttcag caacctcaat				978
Glu Asn Lys Thr Val Val Phe 290				
gaagaaccct taataaac				996
<210> 200				
<211> 293				
<212> PRT				
<213> Helicobacter pylori				
<400> 200				
Met Leu Glu Phe Ile Leu Lys Ile Gln Ala Arg Asp Ser Lys Gly Leu				



[illegible]

<210> 202  
 <211> 259  
 <212> PRT  
 <213> Helicobacter pylori

<400> 202  
 Met Ala Phe Trp His Lys Arg Leu Ala Val Gly Cys Cys Ile Val Leu  
 1 5 10 15  
 Phe Ser Cys Met Met Asn Ala Asn Ser Ile Gln Ile Val Arg Asp Asp  
 20 25 30  
 Pro Pro Leu Asp Pro Thr Leu Pro Ala Trp Val Tyr Ser Val Ala Leu  
 35 40 45  
 Leu Lys Val Tyr Phe Ser Asp Gly Thr Tyr Lys Glu Gly Tyr Ala Thr  
 50 55 60  
 Leu Leu Lys Asn Gly Arg Tyr Ile Ala Ser Ser Glu Thr Leu Tyr Ser  
 65 70 75 80  
 Asn Gly Leu Tyr Pro Lys Thr Ile Leu Ala Lys Met Gln Asp Ser Ser  
 85 90 95  
 Ala Lys Glu Leu Ile Cys Ile Ala Ser Leu Arg Leu Glu Ala Met Asp  
 100 105 110  
 Arg Asn Gln Gly Leu Ser Leu Leu Lys Thr Ala Asp Phe Arg Asp Asp  
 115 120 125  
 Tyr Cys His Lys Arg Glu Glu Ser Tyr Tyr His Ala Arg Ile Tyr Thr  
 130 135 140  
 Lys Tyr Ala Gln Thr Phe His Ser Asn Pro Tyr Thr Asn Gln Lys Thr  
 145 150 155 160  
 Pro Asn Ser Asp Leu Tyr Tyr Pro Ala Leu Asn Glu Gly Asn Ser Phe  
 165 170 175  
 Ser Ile Gln Ile Met Gly Ile Ser Val Ala Glu Leu Leu Lys Ser Lys  
 180 185 190  
 Lys Phe Leu Ser Leu Asp Val Ser Phe Lys Lys Gly Ser Val Leu Trp  
 195 200 205  
 Gly Gly Arg Pro Tyr Phe Ser Glu Val Gly Glu Phe Met Gly Met Ala  
 210 215 220  
 Ser Ser Thr Leu Glu Asn Gln Glu Ser Leu Val Ile Ile Pro Lys Glu  
 225 230 235 240  
 Lys Ile Val Gln Phe Leu Asn Ala Leu Lys Asn Gln Asn Ile Phe Pro  
 245 250 255  
 Asn Ile Pro

<210> 203  
 <211> 669  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (88)...(603)

<400> 203  
 aaaataagga ggaattgttt gattttacga ttggctggag caagcgtttt aacggcttgt 60  
 gtcttttcgg ggtgtttttt tttaaaa atg ttt gat aaa aaa ctt tct agt aac 114  
 Met Phe Asp Lys Lys Leu Ser Ser Asn  
 1 5  
 gat tgg cat atc caa aaa gtg gaa atg aac cat caa gtc tat gac att 162  
 Asp Trp His Ile Gln Lys Val Glu Met Asn His Gln Val Tyr Asp Ile  
 10 15 20 25

gaa acc atg ctc gct gat agc gct ttt aga gag cat gaa gaa gag caa 210  
 Glu Thr Met Leu Ala Asp Ser Ala Phe Arg Glu His Glu Glu Glu Gln  
                     30                    35                    40

gat tcc tct cta aat acc gct ttg cct gaa gat aaa aca gcg att gaa 258  
 Asp Ser Ser Leu Asn Thr Ala Leu Pro Glu Asp Lys Thr Ala Ile Glu  
                     45                    50                    55

gcc aaa gag caa gag caa aaa gaa aaa aga aaa cgc tgg tat gag ctt 306  
 Ala Lys Glu Gln Glu Gln Lys Glu Lys Arg Lys Arg Trp Tyr Glu Leu  
                     60                    65                    70

ttt aaa aag aaa cca aag ccc aaa agc tct atg gga gag ttt gtg ttt 354  
 Phe Lys Lys Lys Pro Lys Pro Lys Ser Ser Met Gly Glu Phe Val Phe  
                     75                    80                    85

gat caa aaa gaa aat cgt att tat ggc aaa ggc tat tgc aac cgg tat 402  
 Asp Gln Lys Glu Asn Arg Ile Tyr Gly Lys Gly Tyr Cys Asn Arg Tyr  
                     90                    95                    100                    105

ttt gcc agc tat gta tgg cag ggc gat agg cac att ggg att gaa gat 450  
 Phe Ala Ser Tyr Val Trp Gln Gly Asp Arg His Ile Gly Ile Glu Asp  
                     110                    115                    120

agc ggg att tca aga aaa gtg tgt aaa gat gag cat tta atg gcg ttt 498  
 Ser Gly Ile Ser Arg Lys Val Cys Lys Asp Glu His Leu Met Ala Phe  
                     125                    130                    135

gaa ttg gaa ttt atg gag aat ttt aag ggt aat ttt acg gta act aag 546  
 Glu Leu Glu Phe Met Glu Asn Phe Lys Gly Asn Phe Thr Val Thr Lys  
                     140                    145                    150

ggc aag gac acg ctc att tta gac aac caa aaa atg aaa att tat ttg 594  
 Gly Lys Asp Thr Leu Ile Leu Asp Asn Gln Lys Met Lys Ile Tyr Leu  
                     155                    160                    165

aaa acg cct tgagtgggtt tttgatttca aaacaatcta agatcactaa 643  
 Lys Thr Pro  
 170

attagggtt aaaaagaaat ttttaa 669

<210> 204  
 <211> 172  
 <212> PRT  
 <213> Helicobacter pylori

<400> 204  
 Met Phe Asp Lys Lys Leu Ser Ser Asn Asp Trp His Ile Gln Lys Val  
   1                    5                    10                    15  
 Glu Met Asn His Gln Val Tyr Asp Ile Glu Thr Met Leu Ala Asp Ser  
                     20                    25                    30  
 Ala Phe Arg Glu His Glu Glu Glu Gln Asp Ser Ser Leu Asn Thr Ala  
                     35                    40                    45  
 Leu Pro Glu Asp Lys Thr Ala Ile Glu Ala Lys Glu Gln Glu Gln Lys  
                     50                    55                    60  
 Glu Lys Arg Lys Arg Trp Tyr Glu Leu Phe Lys Lys Lys Pro Lys Pro  
                     65                    70                    75                    80

Lys Ser Ser Met Gly Glu Phe Val Phe Asp Gln Lys Glu Asn Arg Ile  
85 90 95  
Tyr Gly Lys Gly Tyr Cys Asn Arg Tyr Phe Ala Ser Tyr Val Trp Gln  
100 105 110  
Gly Asp Arg His Ile Gly Ile Glu Asp Ser Gly Ile Ser Arg Lys Val  
115 120 125  
Cys Lys Asp Glu His Leu Met Ala Phe Glu Leu Glu Phe Met Glu Asn  
130 135 140  
Phe Lys Gly Asn Phe Thr Val Thr Lys Gly Lys Asp Thr Leu Ile Leu  
145 150 155 160  
Asp Asn Gln Lys Met Lys Ile Tyr Leu Lys Thr Pro  
165 170

<210> 205  
<211> 290  
<212> DNA  
<213> Helicobacter pylori

<220>  
<221> CDS  
<222> (53)...(235)

<400> 205  
ttgagcttaa gaaacattga taattttgtg gaaaaaggct ctgctttgat ag ata aat 58  
Ile Asn  
1  
  
ttg acg cta acc cct ata aaa cga ttt ttg gag aaa gga aat aat cat 106  
Leu Thr Leu Thr Pro Ile Lys Arg Phe Leu Glu Lys Gly Asn Asn His  
5 10 15  
  
gag agc tac ggc gat aaa aat ctt ttc act ctc atc agc att agc cct 154  
Glu Ser Tyr Gly Asp Lys Asn Leu Phe Thr Leu Ile Ser Ile Ser Pro  
20 25 30  
  
att gct tca tgg ttg ctt gag cat caa ttt aaa aca aat gct acc aga 202  
Ile Ala Ser Trp Leu Leu Glu His Gln Phe Lys Thr Asn Ala Thr Arg  
35 40 45 50  
  
gat cag aac tta cga ttt gaa tgc gag ttc ttt tgaaatcacg caatgcgcta 255  
Asp Gln Asn Leu Arg Phe Glu Cys Glu Phe Phe  
55 60  
  
aacctttgac tgaagtgagg ctcattagta ttttg 290

<210> 206  
<211> 61  
<212> PRT  
<213> Helicobacter pylori

<400> 206  
Ile Asn Leu Thr Leu Thr Pro Ile Lys Arg Phe Leu Glu Lys Gly Asn  
1 5 10 15  
Asn His Glu Ser Tyr Gly Asp Lys Asn Leu Phe Thr Leu Ile Ser Ile  
20 25 30  
Ser Pro Ile Ala Ser Trp Leu Leu Glu His Gln Phe Lys Thr Asn Ala  
35 40 45  
Thr Arg Asp Gln Asn Leu Arg Phe Glu Cys Glu Phe Phe  
50 55 60

**SECRET**

<400> 207

-235-





**090601Z**

<221> CDS

<222> (190) . . . (1299)

<400> 209

-237-

0085513-052901

Lys	Thr	Leu	Ser	Phe	Asn	Lys	Asp	Ala	Leu	Thr	Gln	Gly	Glu	Asp	Tyr	
				195					200					205		
gat	tat	att	aca	agg	act	tcg	caa	aat	caa	ggc	gtt	ttg	caa	act	aca	855
Asp	Tyr	Ile	Thr	Arg	Thr	Ser	Gln	Asn	Gln	Gly	Val	Leu	Gln	Thr	Thr	
			210				215					220				
gga	ttt	gtc	aat	gca	gaa	aat	tta	aac	cca	cca	ttt	act	tgg	agt	tta	903
Gly	Phe	Val	Asn	Ala	Glu	Asn	Leu	Asn	Pro	Pro	Phe	Thr	Trp	Ser	Leu	
		225					230					235				
ggg	ctt	ttg	caa	atg	gat	ttt	ttc	tat	cgt	aaa	aag	tca	tgg	tat	gcg	951
Gly	Leu	Leu	Gln	Met	Asp	Phe	Phe	Tyr	Arg	Lys	Lys	Ser	Trp	Tyr	Ala	
	240					245					250					
gga	caa	ttc	atg	cga	aaa	atc	aca	cca	aaa	act	gaa	att	gaa	aat	aaa	999
Gly	Gln	Phe	Met	Arg	Lys	Ile	Thr	Pro	Lys	Thr	Glu	Ile	Glu	Asn	Lys	
	255				260					265					270	
att	gat	tta	cgc	ata	gcc	aac	tac	ttc	aca	acg	ctt	tta	aac	gcc	tta	1047
Ile	Asp	Leu	Arg	Ile	Ala	Asn	Tyr	Phe	Thr	Thr	Leu	Leu	Asn	Ala	Leu	
				275					280					285		
aaa	cgc	cct	tta	tta	agc	gta	ttg	gtt	aga	gat	att	gat	aaa	act	ttt	1095
Lys	Arg	Pro	Leu	Leu	Ser	Val	Leu	Val	Arg	Asp	Ile	Asp	Lys	Thr	Phe	
			290					295					300			
agg	gag	caa	aaa	atc	caa	cta	ccc	cta	aaa	ccc	acc	gct	aaa	act	caa	1143
Arg	Glu	Gln	Lys	Ile	Gln	Leu	Pro	Leu	Lys	Pro	Thr	Ala	Lys	Thr	Gln	
		305					310					315				
acc	ctt	gat	ggt	att	gat	ttt	gat	ttc	atg	cac	acc	ctt	atc	aac	gcc	1191
Thr	Leu	Asp	Gly	Ile	Asp	Phe	Asp	Phe	Met	His	Thr	Leu	Ile	Asn	Ala	
	320					325					330					
cta	atg	aag	caa	acc	att	caa	ggc	gtg	gct	caa	tac	tgc	gac	gct	aaa	1239
Leu	Met	Lys	Gln	Thr	Ile	Gln	Gly	Val	Ala	Gln	Tyr	Cys	Asp	Ala	Lys	
	335				340				345						350	
ata	caa	gct	aca	aaa	gag	gtt	atc	agc	caa	gaa	gcg	ccc	gtt	caa	aaa	1287
Ile	Gln	Ala	Thr	Lys	Glu	Val	Ile	Ser	Gln	Glu	Ala	Pro	Val	Gln	Lys	
				355					360					365		
gac	tcg	tta	ttt	taaaaggggt	tttaagcgcg	ctagcttgtg	ttacaataaa									1339
Asp	Ser	Leu	Phe													
			370													
cttaaaattc	gcttg															1354
<210>	210															
<211>	370															
<212>	PRT															
<213>	Helicobacter pylori															
<400>	210															
Val	Arg	Ala	Ala	Thr	Asn	Asn	Gly	Ile	Lys	Gly	Phe	Ile	Ile	Asp	Asp	
1				5					10					15		
Pro	Thr	Phe	Ala	Asn	Lys	Lys	Asn	Thr	Leu	Ser	Phe	Ala	Gln	Asp	Thr	
			20					25					30			

Phe Thr Val Phe Tyr Gln Lys Gln Pro Tyr Phe Thr Gly Asn Lys Val  
 35 40 45  
 Lys Ile Leu Lys Pro Lys Phe Ala Phe Lys Ser Pro Lys Ile Leu His  
 50 55 60  
 Ser Ile Ser Ala Ile Leu Gln Phe Ile Leu Lys Pro Leu Thr Trp Gly  
 65 70 75 80  
 Leu Gly Ser Thr Thr Glu Ser Ile Ala Glu Phe Lys Phe Ser Leu Pro  
 85 90 95  
 Leu Lys Pro Thr Ala Asn Ala Gln Thr Leu Glu Asp Ile Asp Phe Asp  
 100 105 110  
 Phe Met Glu Lys Phe Ile Ala Glu Leu Glu Gln Cys Arg Leu Ala Glu  
 115 120 125  
 Leu Glu Gln Cys Arg Leu Ala Glu Leu Gln Ala Tyr Leu Lys Ala Thr  
 130 135 140  
 Gly Leu Glu Asn Thr Thr Leu Ser Asn Asp Glu Glu Asn Ala Leu Asn  
 145 150 155 160  
 Val Phe Asn Asn Ser Gly Gly Gly Gly Gly Asn Thr Pro Cys Gly Leu  
 165 170 175  
 Thr Trp Gln Ser Phe Arg Leu Gly Asp Leu Phe Glu Ile Glu Lys Thr  
 180 185 190  
 Leu Ser Phe Asn Lys Asp Ala Leu Thr Gln Gly Glu Asp Tyr Asp Tyr  
 195 200 205  
 Ile Thr Arg Thr Ser Gln Asn Gln Gly Val Leu Gln Thr Thr Gly Phe  
 210 215 220  
 Val Asn Ala Glu Asn Leu Asn Pro Pro Phe Thr Trp Ser Leu Gly Leu  
 225 230 235 240  
 Leu Gln Met Asp Phe Phe Tyr Arg Lys Lys Ser Trp Tyr Ala Gly Gln  
 245 250 255  
 Phe Met Arg Lys Ile Thr Pro Lys Thr Glu Ile Glu Asn Lys Ile Asp  
 260 265 270  
 Leu Arg Ile Ala Asn Tyr Phe Thr Thr Leu Leu Asn Ala Leu Lys Arg  
 275 280 285  
 Pro Leu Leu Ser Val Leu Val Arg Asp Ile Asp Lys Thr Phe Arg Glu  
 290 295 300  
 Gln Lys Ile Gln Leu Pro Leu Lys Pro Thr Ala Lys Thr Gln Thr Leu  
 305 310 315 320  
 Asp Gly Ile Asp Phe Asp Phe Met His Thr Leu Ile Asn Ala Leu Met  
 325 330 335  
 Lys Gln Thr Ile Gln Gly Val Ala Gln Tyr Cys Asp Ala Lys Ile Gln  
 340 345 350  
 Ala Thr Lys Glu Val Ile Ser Gln Glu Ala Pro Val Gln Lys Asp Ser  
 355 360 365  
 Leu Phe  
 370

<210> 211  
 <211> 450  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (164)...(367)

<400> 211  
 aatccagcat gccctctaata tcaaacacgc cctcttcaag cttgtttatg ccctcttgtt 60  
 ttaagtcgta ttctgcgcta atctcgccca tgatctcttc aatgatgtct tccatagtga 120  
 gcaacccggc tgtgccgccg tattcatcaa tcaccaaagc ggt atg gat ttg ctc 175  
 Met Asp Leu Leu

ttt ttt cat ttt aat aag gat ttg aga aat gga agc gct ttc ggg gac 223  
 Phe Phe His Phe Asn Lys Asp Leu Arg Asn Gly Ser Ala Phe Gly Asp  
 5 10 15 20

gat gat cat ttt cct aac gat ttg att gaa atc atg cat ttt ggg ggt 271  
 Asp Asp His Phe Pro Asn Asp Leu Ile Glu Ile Met His Phe Gly Gly  
 25 30 35

aaa aat aga gcg cga aag caa atc cct aat atg cac cat gcc gat aat 319  
 Lys Asn Arg Ala Arg Lys Gln Ile Pro Asn Met His His Ala Asp Asn  
 40 45 50

gtt atc ctt aga acc ctt gca ata agg gta gcg cgt gaa atg gcc ttt 367  
 Val Ile Leu Arg Thr Leu Ala Ile Arg Val Ala Arg Glu Met Ala Phe  
 55 60 65

taaaacaatg tctatatatttt cttcatagct gttttcttca tccaaacaca ccatgtcttt 427  
 tcgtgggggc atgatttctt tag 450

<210> 212  
 <211> 68  
 <212> PRT  
 <213> Helicobacter pylori

<400> 212  
 Met Asp Leu Leu Phe Phe His Phe Asn Lys Asp Leu Arg Asn Gly Ser  
 1 5 10 15  
 Ala Phe Gly Asp Asp Asp His Phe Pro Asn Asp Leu Ile Glu Ile Met  
 20 25 30  
 His Phe Gly Gly Lys Asn Arg Ala Arg Lys Gln Ile Pro Asn Met His  
 35 40 45  
 His Ala Asp Asn Val Ile Leu Arg Thr Leu Ala Ile Arg Val Ala Arg  
 50 55 60  
 Glu Met Ala Phe  
 65

<210> 213  
 <211> 1051  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (51)...(998)

<400> 213  
 accaagaggt cgtaaagc tattaccaac atttaaaaca aggataaaac atg caa 56  
 Met Gln  
 1

gaa ttc agt ttg tgg tgc gat ttt ata gaa agg gat ttt tta gaa aac 104  
 Glu Phe Ser Leu Trp Cys Asp Phe Ile Glu Arg Asp Phe Leu Glu Asn  
 5 10 15

gac ttt tta aag ctc att aat aag ggg gct att tgc ggg gca acg agt 152  
 Asp Phe Leu Lys Leu Ile Asn Lys Gly Ala Ile Cys Gly Ala Thr Ser  
 20 25 30

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aac cct agt ttg ttt tgc gaa gcg atc aca aaa agc gcg ttt tat aaa	200
Asn Pro Ser Leu Phe Cys Glu Ala Ile Thr Lys Ser Ala Phe Tyr Lys	
35 40 45 50	
gat gaa atc gct aaa ctc aaa ggc aaa aaa gct aaa gaa att tat gaa	248
Asp Glu Ile Ala Lys Leu Lys Gly Lys Lys Ala Lys Glu Ile Tyr Glu	
55 60 65	
act ctg gcg tta aag gat att tta caa gct tct agc gcg ttg atg cct	296
Thr Leu Ala Leu Lys Asp Ile Leu Gln Ala Ser Ser Ala Leu Met Pro	
70 75 80	
tta tat gaa aaa gac cct aac aat ggc tac att agc cta gaa att gac	344
Leu Tyr Glu Lys Asp Pro Asn Asn Gly Tyr Ile Ser Leu Glu Ile Asp	
85 90 95	
cct ttt tta gaa gat gat gcc gct aaa agc att gat gaa gcc aag cgg	392
Pro Phe Leu Glu Asp Asp Ala Ala Lys Ser Ile Asp Glu Ala Lys Arg	
100 105 110	
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Leu Phe Lys Thr Leu Asn Arg Pro Asn Val Met Ile Lys Val Pro Ala	
115 120 125 130	
agt gaa agc ggg att gaa gtg gtt agc gct tta act caa gcc tct att	488
Ser Glu Ser Gly Ile Glu Val Val Ser Ala Leu Thr Gln Ala Ser Ile	
135 140 145	
cct gtt aat gta act tta gtc ttt tcg cct aaa att gcc ggt gaa atc	536
Pro Val Asn Val Thr Leu Val Phe Ser Pro Lys Ile Ala Gly Glu Ile	
150 155 160	
gct caa atc tta gcc aaa gaa gcg caa aaa aga gcg gtc att agc gtg	584
Ala Gln Ile Leu Ala Lys Glu Ala Gln Lys Arg Ala Val Ile Ser Val	
165 170 175	
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Phe Val Ser Arg Phe Asp Lys Glu Ile Asp Pro Leu Val Pro Lys Asn	
180 185 190	
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Leu Gln Ala Gln Ser Gly Ile Ile Asn Ala Thr Glu Cys Tyr Tyr Gln	
195 200 205 210	
att aat cag cat gcc aat aag cta aca agc acc ctt ttt gca tcc aca	728
Ile Asn Gln His Ala Asn Lys Leu Thr Ser Thr Leu Phe Ala Ser Thr	
215 220 225	
ggc gtt aaa tcc aat tct tta gct aaa gat tac tac att aaa gcg ctg	776
Gly Val Lys Ser Asn Ser Leu Ala Lys Asp Tyr Tyr Ile Lys Ala Leu	
230 235 240	
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Cys Phe Lys Asn Ser Ile Asn Thr Ala Pro Leu Glu Ala Leu Asn Ala	
245 250 255	
tat ttg ctt gac cca aac acc gag tgt caa acc cct tta aag act aca	872
Tyr Leu Leu Asp Pro Asn Thr Glu Cys Gln Thr Pro Leu Lys Thr Thr	

260

265

270

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 275 280 285 290

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 295 300 305

caa tcc ttt gaa aag ctt tta agc agt ttt tgattttttaa gggtttttttg 1018  
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<211> 316

<212> PRT

<213> Helicobacter pylori

<400> 214

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 Thr Ser Asn Pro Ser Leu Phe Cys Glu Ala Ile Thr Lys Ser Ala Phe  
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 Tyr Lys Asp Glu Ile Ala Lys Leu Lys Gly Lys Lys Ala Lys Glu Ile  
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 65 70 75 80  
 Met Pro Leu Tyr Glu Lys Asp Pro Asn Asn Gly Tyr Ile Ser Leu Glu  
 85 90 95  
 Ile Asp Pro Phe Leu Glu Asp Asp Ala Ala Lys Ser Ile Asp Glu Ala  
 100 105 110  
 Lys Arg Leu Phe Lys Thr Leu Asn Arg Pro Asn Val Met Ile Lys Val  
 115 120 125  
 Pro Ala Ser Glu Ser Gly Ile Glu Val Val Ser Ala Leu Thr Gln Ala  
 130 135 140  
 Ser Ile Pro Val Asn Val Thr Leu Val Phe Ser Pro Lys Ile Ala Gly  
 145 150 155 160  
 Glu Ile Ala Gln Ile Leu Ala Lys Glu Ala Gln Lys Arg Ala Val Ile  
 165 170 175  
 Ser Val Phe Val Ser Arg Phe Asp Lys Glu Ile Asp Pro Leu Val Pro  
 180 185 190  
 Lys Asn Leu Gln Ala Gln Ser Gly Ile Ile Asn Ala Thr Glu Cys Tyr  
 195 200 205  
 Tyr Gln Ile Asn Gln His Ala Asn Lys Leu Thr Ser Thr Leu Phe Ala  
 210 215 220  
 Ser Thr Gly Val Lys Ser Asn Ser Leu Ala Lys Asp Tyr Tyr Ile Lys  
 225 230 235 240  
 Ala Leu Cys Phe Lys Asn Ser Ile Asn Thr Ala Pro Leu Glu Ala Leu  
 245 250 255  
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 260 265 270  
 Thr Thr Glu Ile Glu Ala Phe Lys Lys Glu Leu Lys Val His Asn Ile  
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305 310 315

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Leu Asn Phe Met Thr Lys Lys Lys Asn Arg Met Gln Asp Cys Lys Met  
5 10 15

gtt tgt aaa aat ttt aat cgt aag gaa tct gtt ttg ata gct caa tct 153  
Val Cys Lys Asn Phe Asn Arg Lys Glu Ser Val Leu Ile Ala Gln Ser  
20 25 30

tta gat att tct aaa aaa ggt tcg gta att tta ggc gct ctt ttg agt 201  
Leu Asp Ile Ser Lys Lys Gly Ser Val Ile Leu Gly Ala Leu Leu Ser  
35 40 45

tcg tta tgg ctg aca aac ccc tta aat gcc cat gaa aag aat ggc gcg 249  
Ser Leu Trp Leu Thr Asn Pro Leu Asn Ala His Glu Lys Asn Gly Ala  
50 55 60 65

ttt gtg ggg att agc ttg gaa gtg ggt agg gcc gat caa aag aca aac 297  
Phe Val Gly Ile Ser Leu Glu Val Gly Arg Ala Asp Gln Lys Thr Asn  
70 75 80

gct tat aaa aac ggc gag ttg ttt caa gtg cct ttt ggc gat gtt tcg 345  
Ala Tyr Lys Asn Gly Glu Leu Phe Gln Val Pro Phe Gly Asp Val Ser  
85 90 95

gct aat gat gat ggc aaa gtt cct gac ggg cag acc ggt ggc tgt cag 393  
Ala Asn Asp Asp Gly Lys Val Pro Asp Gly Gln Thr Gly Gly Cys Gln  
100 105 110

cca gct tca ggg acg cca gga acg cca ggc tac act aaa gct aac tgc 441  
Pro Ala Ser Gly Thr Pro Gly Thr Pro Gly Tyr Thr Lys Ala Asn Cys  
115 120 125

gtg gtc aat tgg act tcg cgc acc atg ctt agc acc aat aaa aac att 489  
Val Val Asn Trp Thr Ser Arg Thr Met Leu Ser Thr Asn Lys Asn Ile  
130 135 140 145

cct ggc cgt aac cag ccg atg tat ggg cta ggc gtg atg aca ggc tat 537  
Pro Gly Arg Asn Gln Pro Met Tyr Gly Leu Gly Val Met Thr Gly Tyr  
150 155 160

aag cat ttt atc ggt aaa aaa aga tgg ttt ggg ttg cgc tat tac ggc 585

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Lys	His	Phe	Ile	Gly	Lys	Lys	Arg	Trp	Phe	Gly	Leu	Arg	Tyr	Tyr	Gly		
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Phe	Phe	Asp	Tyr	Gly	His	Thr	Asn	Phe	Ser	Asn	Ser	Arg	Ala	Ala	Asn		
			180					185							190		
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Ala	Ile	Ser	Pro	Phe	Tyr	Leu	Ser	Asp	Gln	Lys	Ala	Asp	Met	Tyr	Thr		
			195					200							205		
tat	ggt	ttt	ggc	aca	gac	atg	ctt	ttt	aac	att	ata	gat	aag	cct	aaa		729
Tyr	Gly	Phe	Gly	Thr	Asp	Met	Leu	Phe	Asn	Ile	Ile	Asp	Lys	Pro	Lys		
						215									225		
gcc	acg	gcc	ggg	ttt	ttt	tta	ggc	gtg	aat	ttt	gcg	ggt	aac	act	tgg		777
Ala	Thr	Ala	Gly	Phe	Phe	Leu	Gly	Val	Asn	Phe	Ala	Gly	Asn	Thr	Trp		
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act	aat	aat	cgt	gtg	ggg	tat	ttt	aag	gac	ggg	tat	gtt	tat	ggc	gtc		825
Thr	Asn	Asn	Arg	Val	Gly	Tyr	Phe	Lys	Asp	Gly	Tyr	Val	Tyr	Gly	Val		
						245									255		
aat	acg	gac	gct	gac	gct	tac	atg	act	aac	gct	gat	ggc	aca	atc	act		873
Asn	Thr	Asp	Ala	Asp	Ala	Tyr	Met	Thr	Asn	Ala	Asp	Gly	Thr	Ile	Thr		
						260									270		
tgc	ggg	gac	acg	acg	ccg	gcg	agt	tgc	aat	gtg	ggg	att	aac	cct	aat		921
Cys	Gly	Asp	Thr	Thr	Pro	Ala	Ser	Cys	Asn	Val	Gly	Ile	Asn	Pro	Asn		
						280									285		
agc	gtc	tat	acc	aca	gga	aaa	ttg	aac	gct	aag	gtg	aat	cac	acg	att		969
Ser	Val	Tyr	Thr	Thr	Gly	Lys	Leu	Asn	Ala	Lys	Val	Asn	His	Thr	Ile		
						295									305		
ttc	caa	ttt	tta	gtg	aat	gtg	ggc	att	aga	act	aat	att	ttt	gaa	cac		1017
Phe	Gln	Phe	Leu	Val	Asn	Val	Gly	Ile	Arg	Thr	Asn	Ile	Phe	Glu	His		
						310									320		
cat	ggc	att	gag	ttt	ggc	atc	aaa	atc	ccc	acg	ctc	cct	aac	tac	ttt		1065
His	Gly	Ile	Glu	Phe	Gly	Ile	Lys	Ile	Pro	Thr	Leu	Pro	Asn	Tyr	Phe		
						325									335		
ttc	aaa	ggt	tct	act	acc	ata	aga	gcg	aaa	aaa	caa	ggc	ccg	cta	gag		1113
Phe	Lys	Gly	Ser	Thr	Thr	Ile	Arg	Ala	Lys	Lys	Gln	Gly	Pro	Leu	Glu		
						340									350		
aat	ggc	caa	cca	acc	act	atc	acc	gga	gca	gaa	acc	aat	ttc	agc	tta		1161
Asn	Gly	Gln	Pro	Thr	Thr	Ile	Thr	Gly	Ala	Glu	Thr	Asn	Phe	Ser	Leu		
						355									365		
acc	caa	acc	tta	cgc	cgt	cag	tat	tct	atg	tat	ttg	cgc	tat	gtt	tat		1209
Thr	Gln	Thr	Leu	Arg	Arg	Gln	Tyr	Ser	Met	Tyr	Leu	Arg	Tyr	Val	Tyr		
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Thr	Phe																



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 <213> Helicobacter pylori

<400> 216

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Ser	Leu	Asp	Ile	Ser	Lys	Lys	Gly	Ser	Val	Ile	Leu	Gly	Ala	Leu	Leu
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Ser	Ser	Leu	Trp	Leu	Thr	Asn	Pro	Leu	Asn	Ala	His	Glu	Lys	Asn	Gly
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Ala	Phe	Val	Gly	Ile	Ser	Leu	Glu	Val	Gly	Arg	Ala	Asp	Gln	Lys	Thr
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Asn	Ala	Tyr	Lys	Asn	Gly	Glu	Leu	Phe	Gln	Val	Pro	Phe	Gly	Asp	Val
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Ser	Ala	Asn	Asp	Asp	Gly	Lys	Val	Pro	Asp	Gly	Gln	Thr	Gly	Gly	Cys
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Gln	Pro	Ala	Ser	Gly	Thr	Pro	Gly	Thr	Pro	Gly	Tyr	Thr	Lys	Ala	Asn
			115				120						125		
Cys	Val	Val	Asn	Trp	Thr	Ser	Arg	Thr	Met	Leu	Ser	Thr	Asn	Lys	Asn
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Tyr	Lys	His	Phe	Ile	Gly	Lys	Lys	Arg	Trp	Phe	Gly	Leu	Arg	Tyr	Tyr
				165					170						175
Gly	Phe	Phe	Asp	Tyr	Gly	His	Thr	Asn	Phe	Ser	Asn	Ser	Arg	Ala	Ala
			180					185					190		
Asn	Ala	Ile	Ser	Pro	Phe	Tyr	Leu	Ser	Asp	Gln	Lys	Ala	Asp	Met	Tyr
			195				200					205			
Thr	Tyr	Gly	Phe	Gly	Thr	Asp	Met	Leu	Phe	Asn	Ile	Ile	Asp	Lys	Pro
						215					220				
Lys	Ala	Thr	Ala	Gly	Phe	Phe	Leu	Gly	Val	Asn	Phe	Ala	Gly	Asn	Thr
225					230					235					240
Trp	Thr	Asn	Asn	Arg	Val	Gly	Tyr	Phe	Lys	Asp	Gly	Tyr	Val	Tyr	Gly
				245					250					255	
Val	Asn	Thr	Asp	Ala	Asp	Ala	Tyr	Met	Thr	Asn	Ala	Asp	Gly	Thr	Ile
			260					265					270		
Thr	Cys	Gly	Asp	Thr	Thr	Pro	Ala	Ser	Cys	Asn	Val	Gly	Ile	Asn	Pro
		275					280					285			
Asn	Ser	Val	Tyr	Thr	Thr	Gly	Lys	Leu	Asn	Ala	Lys	Val	Asn	His	Thr
		290				295					300				
Ile	Phe	Gln	Phe	Leu	Val	Asn	Val	Gly	Ile	Arg	Thr	Asn	Ile	Phe	Glu
305					310					315					320
His	His	Gly	Ile	Glu	Phe	Gly	Ile	Lys	Ile	Pro	Thr	Leu	Pro	Asn	Tyr
				325					330					335	
Phe	Phe	Lys	Gly	Ser	Thr	Thr	Ile	Arg	Ala	Lys	Lys	Gln	Gly	Pro	Leu
			340					345					350		
Glu	Asn	Gly	Gln	Pro	Thr	Thr	Ile	Thr	Gly	Ala	Glu	Thr	Asn	Phe	Ser
		355					360					365			
Leu	Thr	Gln	Thr	Leu	Arg	Arg	Gln	Tyr	Ser	Met	Tyr	Leu	Arg	Tyr	Val
		370				375					380				
Tyr	Thr	Phe													
385															

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09895913-06901

<212> DNA  
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<220>  
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<222> (47)...(481)

<400> 217

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Ile Tyr Pro Tyr Val Leu Val Val His Leu Leu Cys Ala Ile Ile Phe
   5                               10                               15

att ggc tac ttg ttt ttt gat ggg gta att ttc cct aat gtg aag aaa      151
Ile Gly Tyr Leu Phe Phe Asp Gly Val Ile Phe Pro Asn Val Lys Lys
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atg ttt ggc gaa gag ttt gcc aat aaa gcg aat aca gga atc act caa      199
Met Phe Gly Glu Glu Phe Ala Asn Lys Ala Asn Thr Gly Ile Thr Gln
                               40                               45                               50

aga gcg atc aaa atc atg ccc tta tgc gtt tta ggg ctt gtt tta aca      247
Arg Ala Ile Lys Ile Met Pro Leu Cys Val Leu Gly Leu Val Leu Thr
                               55                               60                               65

ggg ggc atg atg ctt agc caa tac atg ggg ggc gat aaa ggc tgg tgt      295
Gly Gly Met Met Leu Ser Gln Tyr Met Gly Gly Asp Lys Gly Trp Cys
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gaa acc cct ttt caa aag ata ctc atg ctt aaa gtg atc tta gcg tta      343
Glu Thr Pro Phe Gln Lys Ile Leu Met Leu Lys Val Ile Leu Ala Leu
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agc att ttt ctt ttg gtg ctt ttt tct tta tcg tgt aag ttt ttg ggc      391
Ser Ile Phe Leu Leu Val Leu Phe Ser Leu Ser Cys Lys Phe Leu Gly
 100                               105                               110                               115

aag aaa aac cct att ggt aaa tat atc cac cct atc gct cta act ttt      439
Lys Lys Asn Pro Ile Gly Lys Tyr Ile His Pro Ile Ala Leu Thr Phe
   120                               125                               130

ggc ttt tta atc gcc att tta gcc aaa acg atg tgg ttt gtt      481
Gly Phe Leu Ile Ala Ile Leu Ala Lys Thr Met Trp Phe Val
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<213> Helicobacter pylori

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Ile Ile Phe Ile Gly Tyr Leu Phe Phe Asp Gly Val Ile Phe Pro Asn

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gcg cac cag cat ttt gag act tta agg gcg cgt ttt gaa aat ttt ggc Ala His Gln His Phe Glu Thr Leu Arg Ala Arg Phe Glu Asn Phe Gly 550 555 560	1736
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gaa gag cat aaa ttt ggc gtg aaa caa aaa gaa gct tta aaa gaa ttg Glu Glu His Lys Phe Gly Val Lys Gln Lys Glu Ala Leu Lys Glu Leu 610 615 620 625	1928
agt aag agc gtg cat ttt tta agc atg tcc gct acg cct atc ccg cgc Ser Lys Ser Val His Phe Leu Ser Met Ser Ala Thr Pro Ile Pro Arg 630 635 640	1976
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acc ccg ccc aca gac aga aag ccc agc cgc act ttt ttg aaa gaa aag Thr Pro Pro Thr Asp Arg Lys Pro Ser Arg Thr Phe Leu Lys Glu Lys 660 665 670	2072
aat gac gaa ctc tta aaa gag att att tac aga gaa tta cgc cgt aac Asn Asp Glu Leu Leu Lys Glu Ile Ile Tyr Arg Glu Leu Arg Arg Asn 675 680 685	2120
ggg caa att ttt tac atc cat aac cac atc gct agc att tta aaa gtc Gly Gln Ile Phe Tyr Ile His Asn His Ile Ala Ser Ile Leu Lys Val 690 695 700 705	2168
aaa acc aag cta gaa gat tta atc cct aaa ctc aaa atc gct att ttg Lys Thr Lys Leu Glu Asp Leu Ile Pro Lys Leu Lys Ile Ala Ile Leu 710 715 720	2216
cat tcc cag att aac gct aat gag agc gaa gaa atc atg cta gag ttt His Ser Gln Ile Asn Ala Asn Glu Ser Glu Glu Ile Met Leu Glu Phe 725 730 735	2264
gcc aag gga aat tat cag gtt tta tta tgc act tct att gtg gaa tca Ala Lys Gly Asn Tyr Gln Val Leu Leu Cys Thr Ser Ile Val Glu Ser 740 745 750	2312
ggg att cat ttg cct aac gct aac acg atc att ata gat aat gcg caa Gly Ile His Leu Pro Asn Ala Asn Thr Ile Ile Ile Asp Asn Ala Gln	2360

765

**06-09-2017**

3101

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<212> PRT
<213> Helicobacter pylori
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Val	Ile	Ser 35	Tyr	Phe	Lys	Pro	Asn 40	Thr	Lys	Ala	Ile	Leu 45	Phe	Pro	Glu
Phe	Arg 50	Ala	Lys	Lys	Asn	Asp 55	Leu	Arg	Ser	Phe 60	Glu	Glu	Phe		
Leu 65	Gln	Leu	Leu	Gly 70	Gly	Leu	Arg	Glu	Phe 75	Tyr	Gln	Ala	Leu	Glu	Asn 80
Lys	Gln	Glu	Thr	Ile 85	Ile	Ile	Ala	Pro	Ile 90	Ser	Ala	Leu	Leu	His 95	Pro
Leu	Pro	Lys	Lys 100	Glu	Leu	Leu	Glu	Ser 105	Phe	Lys	Ile	Thr	Leu 110	Leu	Glu
Lys	Tyr	Asn 115	Leu	Lys	Asp	Leu	Lys 120	Asp	Lys	Leu	Phe	Tyr 125	Tyr	Gly	Tyr
Glu	Ile 130	Leu	Asp	Leu	Val	Glu 135	Val	Glu	Gly	Glu	Ala 140	Ser	Phe	Arg	Gly
Asp 145	Ile	Val	Asp	Ile 150	Tyr	Ala	Pro	Asn	Ser	Lys 155	Ala	Tyr	Arg	Leu	Ser 160
Phe	Phe	Asp	Thr	Glu 165	Cys	Glu	Ser	Ile	Lys 170	Glu	Phe	Asp	Pro	Ile 175	Thr
Gln	Met	Ser	Leu 180	Lys	Glu	Asp	Leu	Leu 185	Glu	Ile	Glu	Ile	Pro 190	Pro	Thr
Leu	Phe	Ser 195	Leu	Asp	Glu	Ser	Ser 200	Tyr	Lys	Asp	Leu	Lys 205	Thr	Lys	Val
Glu	Gln 210	Ser	Pro	Leu	Asn	Ser 215	Phe	Ser	Lys	Asp	Leu	Thr 220	Ser	Phe	Gly
Leu 225	Trp	Phe	Leu	Gly 230	Glu	Lys	Ala	Gln	Asp	Leu 235	Leu	Ile	Val	Tyr	Lys 240
Ser	Ile	Ile	Ser	Pro 245	Arg	Ala	Leu	Glu	Glu 250	Ile	Gln	Glu	Leu	Ala 255	Ser
Leu	Asn	Glu	Leu 260	Asp	Cys	Glu	Arg	Phe 265	Lys	Phe	Leu	Lys 270	Val	Leu	Glu
Asn	Ala	Gln 275	Gly	Tyr	Glu	Asp	Leu	Glu 280	Ile	His	Ala	His 285	Ala	Leu	Glu
Gly	Phe 290	Ile	Ala	Leu	His	Ser 295	Asn	His	Lys	Ile	Thr 300	Leu	Leu	Ala	Pro
Asn 305	Lys	Thr	Ile	Leu	Asp 310	Asn	Ala	Ile	Ser	Ala 315	Leu	Asp	Ala	Gly	Asn 320
Met	Glu	Cys	Val	Ile 325	Ala	Pro	Phe	Val	Leu 330	Asn	Phe	Lys	Thr	Pro	Asp
Gly	Ile	Phe	Ile	Ser 340	Leu	Asn	Ser	Phe 345	Glu	Arg	Lys	Lys	Lys	Arg	Gln
Lys	Ser	Lys 355	Leu	Ala	Leu	Asn	Glu 360	Leu	Asn	Pro	Gly	Glu 365	Trp	Val	Val
His	Asp 370	Asp	Tyr	Gly	Val	Gly 375	Val	Phe	Ser	Gln	Leu	Val 380	Gln	His	Ser

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Val	Leu	Gly	Ser	Lys	Arg	Asp	Phe	Leu	Glu	Ile	Ala	Tyr	Leu	Gly	Glu
385					390					395					400
Asp	Lys	Leu	Leu	Leu	Pro	Val	Glu	Asn	Leu	His	Leu	Ile	Ala	Arg	Tyr
				405					410						415
Val	Ala	Gln	Ser	Asp	Ser	Val	Pro	Ala	Lys	Asp	Arg	Leu	Gly	Lys	Gly
			420					425					430		
Ser	Phe	Leu	Lys	Leu	Lys	Ala	Lys	Val	Arg	Thr	Lys	Leu	Leu	Glu	Ile
		435					440					445			
Ala	Ser	Lys	Ile	Ile	Glu	Leu	Ala	Ala	Glu	Arg	Asn	Leu	Ile	Leu	Gly
	450					455					460				
Lys	Lys	Met	Asp	Val	His	Leu	Ala	Glu	Leu	Glu	Val	Phe	Lys	Ser	His
465					470					475					480
Ala	Gly	Phe	Glu	Tyr	Thr	Ser	Asp	Gln	Glu	Lys	Ala	Ile	Ala	Glu	Ile
				485					490						495
Ser	Lys	Asp	Leu	Ser	Ser	His	Arg	Val	Met	Asp	Arg	Leu	Leu	Ser	Gly
			500					505					510		
Asp	Val	Gly	Phe	Gly	Lys	Thr	Glu	Val	Ala	Met	His	Ala	Ile	Phe	Cys
		515					520					525			
Ala	Phe	Leu	Asn	Gly	Phe	Gln	Ser	Ala	Leu	Val	Val	Pro	Thr	Thr	Leu
	530					535					540				
Leu	Ala	His	Gln	His	Phe	Glu	Thr	Leu	Arg	Ala	Arg	Phe	Glu	Asn	Phe
545					550					555					560
Gly	Val	Lys	Val	Ala	Arg	Leu	Asp	Arg	Tyr	Ala	Ser	Glu	Lys	Asn	Lys
				565					570						575
Leu	Leu	Lys	Ala	Val	Glu	Leu	Gly	Gln	Val	Asp	Ala	Leu	Ile	Gly	Thr
			580					585					590		
His	Ala	Ile	Leu	Gly	Ala	Lys	Phe	Lys	Asn	Leu	Gly	Leu	Val	Val	Val
		595					600					605			
Asp	Glu	Glu	His	Lys	Phe	Gly	Val	Lys	Gln	Lys	Glu	Ala	Leu	Lys	Glu
	610					615					620				
Leu	Ser	Lys	Ser	Val	His	Phe	Leu	Ser	Met	Ser	Ala	Thr	Pro	Ile	Pro
625					630					635					640
Arg	Thr	Leu	Asn	Met	Ala	Leu	Ser	Gln	Ile	Lys	Gly	Ile	Ser	Ser	Leu
				645					650					655	
Lys	Thr	Pro	Pro	Thr	Asp	Arg	Lys	Pro	Ser	Arg	Thr	Phe	Leu	Lys	Glu
			660					665					670		
Lys	Asn	Asp	Glu	Leu	Leu	Lys	Glu	Ile	Ile	Tyr	Arg	Glu	Leu	Arg	Arg
		675					680					685			
Asn	Gly	Gln	Ile	Phe	Tyr	Ile	His	Asn	His	Ile	Ala	Ser	Ile	Leu	Lys
	690					695					700				
Val	Lys	Thr	Lys	Leu	Glu	Asp	Leu	Ile	Pro	Lys	Leu	Lys	Ile	Ala	Ile
705					710					715					720
Leu	His	Ser	Gln	Ile	Asn	Ala	Asn	Glu	Ser	Glu	Glu	Ile	Met	Leu	Glu
				725					730					735	
Phe	Ala	Lys	Gly	Asn	Tyr	Gln	Val	Leu	Leu	Cys	Thr	Ser	Ile	Val	Glu
			740					745					750		
Ser	Gly	Ile	His	Leu	Pro	Asn	Ala	Asn	Thr	Ile	Ile	Ile	Asp	Asn	Ala
		755					760						765		
Gln	Asn	Phe	Gly	Leu	Ala	Asp	Leu	His	Gln	Leu	Arg	Gly	Arg	Val	Gly
	770					775					780				
Arg	Gly	Lys	Lys	Glu	Gly	Phe	Cys	Tyr	Phe	Leu	Ile	Glu	Asp	Gln	Lys
785					790					795					800
Ser	Leu	Asn	Glu	Gln	Ala	Leu	Lys	Arg	Leu	Leu	Ala	Leu	Glu	Lys	Asn
				805					810					815	
Ser	Tyr	Leu	Gly	Ser	Gly	Glu	Ser	Val	Ala	Tyr	His	Asp	Leu	Glu	Ile
			820					825					830		
Arg	Gly	Gly	Gly	Asn	Leu	Leu	Gly	Gln	Asp	Gln	Ser	Gly	His	Ile	Lys
		835					840					845			
Asn	Ile	Gly	Tyr	Ala	Leu	Tyr	Thr	Arg	Met	Leu	Glu	Asp	Ala	Ile	Tyr

850	Glu Leu Ser Gly Gly Lys Lys Arg Leu Glu Lys Ser Val Glu Ile Gln	855		860	
865	Leu Gly Val Ser Ala Phe Leu Asn Pro Glu Leu Ile Ala Ser Asp Ser	870		875	880
		885		890	895
Leu Arg Leu Asp Leu Tyr Arg Arg Leu Ser Leu Cys Glu Asn Thr Asp					
		900		905	910
Glu Val Gly Gln Ile His Glu Glu Ile Glu Asp Arg Phe Gly Lys Ile					
		915		920	925
Asp Asp Leu Ser Ala Gln Phe Leu Gln Ile Ile Thr Leu Lys Ile Leu					
		930		935	940
Ala Asn Gln Leu Gly Ile Ile Lys Leu Ser Asn Phe Asn Gln Asn Ile					
945		950		955	960
Thr Ile Thr Tyr Ser Asp Glu Lys Lys Glu Ser Leu Lys Ala Pro Ser					
		965		970	975
Lys Asp Asp Asn Asp Ile Leu Glu Thr Leu Leu Lys His Leu Arg Ala					
		980		985	990
Gln Ile Ser Leu Lys Arg Arg					
995					

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 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (46)...(1161)

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	Met Gln His Glu
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atc cct att gcc ttt gcc ttt gat aaa aac tac cta aaa aca ggg gct	105
Ile Pro Ile Ala Phe Ala Phe Asp Lys Asn Tyr Leu Lys Thr Gly Ala	
5 10 15 20	
gtg gct ctc tac tct tta ttg cat gcc cat cgt gca gtt gaa ggg gta	153
Val Ala Leu Tyr Ser Leu Leu His Ala His Arg Ala Val Glu Gly Val	
25 30 35	
ttt ttc agt atc tat ata ttc tat agc ggt ttg aat gaa gat gat tta	201
Phe Phe Ser Ile Tyr Ile Phe Tyr Ser Gly Leu Asn Glu Asp Asp Leu	
40 45 50	
aac agg ctc caa gaa act atc aaa cct ttc aaa cat ttt gcc gct tta	249
Asn Arg Leu Gln Glu Thr Ile Lys Pro Phe Lys His Phe Ala Ala Leu	
55 60 65	
aaa tgc caa gat att agc gcc act ctt gat tct ttg ccc acc atc acg	297
Lys Cys Gln Asp Ile Ser Ala Thr Leu Asp Ser Leu Pro Thr Ile Thr	
70 75 80	
gat agt gca tgg gtt aat cgc tat tct aga atg att ttg gtc aaa tac	345
Asp Ser Ala Trp Val Asn Arg Tyr Ser Arg Met Ile Leu Val Lys Tyr	
85 90 95 100	
ctt ctc cct agt tta ttc ccc caa tac agc aaa atg att tgg tct gat	393

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Leu	Leu	Pro	Ser	Leu	Phe	Pro	Gln	Tyr	Ser	Lys	Met	Ile	Trp	Ser	Asp	
				105					110					115		
gtg	gat	gtg	gtc	ttt	tgc	aga	gct	ttc	gct	gat	gat	ttt	atc	gct	tta	441
Val	Asp	Val	Val	Phe	Cys	Arg	Ala	Phe	Ala	Asp	Asp	Phe	Ile	Ala	Leu	
				120				125					130			
gac	aca	agc	gaa	tct	ttt	cat	ttg	agt	ggg	gtg	ata	agt	tta	gta	tca	489
Asp	Thr	Ser	Glu	Ser	Phe	His	Leu	Ser	Gly	Val	Ile	Ser	Leu	Val	Ser	
			135				140					145				
caa	tca	gtt	aca	gag	ggg	ttt	tgg	ttt	tgc	aat	ttg	gat	tac	atg	cga	537
Gln	Ser	Val	Thr	Glu	Gly	Phe	Trp	Phe	Cys	Asn		Leu	Asp	Tyr	Met	
			150				155				160					
aag	cac	tct	ttc	acc	caa	cag	gtc	tta	gaa	aaa	ttt	aaa	att	caa	gta	585
Lys	His	Ser	Phe	Thr	Gln	Gln	Val	Leu	Glu	Lys	Phe	Lys	Ile	Gln	Val	
					170					175					180	
atg	cgt	cca	tat	ttt	aaa	gaa	cct	aca	tta	ata	cac	cat	ttg	cat	gct	633
Met	Arg	Pro	Tyr	Phe	Lys	Glu	Pro	Thr	Leu	Ile	His	His	Leu	His	Ala	
				185					190					195		
tat	att	aaa	gaa	ctt	ccc	tta	cac	tat	tgc	gtt	ctg	cct	tat	tat	tat	681
Tyr	Ile	Lys	Glu	Leu	Pro	Leu	His	Tyr	Cys	Val	Leu	Pro	Tyr	Tyr	Tyr	
			200					205					210			
caa	gaa	gaa	ctt	gat	gat	ttg	aga	cat	aaa	gct	tcc	tta	ccc	att	cgg	729
Gln	Glu	Glu	Leu	Asp	Asp	Leu	Arg	His	Lys	Ala	Ser	Leu	Pro	Ile	Arg	
			215				220					225				
ttt	gaa	atc	atc	cac	caa	gac	aaa	ccc	aat	gaa	ttt	atc	cat	cgc	cag	777
Phe	Glu	Ile	Ile	His	Gln	Asp	Lys	Pro	Asn	Glu	Phe	Ile	His	Arg	Gln	
		230				235					240					
caa	atc	ccc	tat	gag	atc	tct	caa	att	caa	aac	att	ctt	tca	aac	cct	825
Gln	Ile	Pro	Tyr	Glu	Ile	Ser	Gln	Ile	Gln	Asn	Ile	Leu	Ser	Asn	Pro	
				245		250				255					260	
att	atc	atg	cac	tat	gaa	tct	gat	aaa	gat	gct	ctt	gga	atc	tac	aat	873
Ile	Ile	Met	His	Tyr	Glu	Ser	Asp	Lys	Asp	Ala	Leu	Gly	Ile	Tyr	Asn	
				265					270				275			
ggc	aaa	cct	tgg	gag	ttc	cct	ttg	ggg	aat	caa	tac	cac	ctg	tgg	tta	921
Gly	Lys	Pro	Trp	Glu	Phe	Pro	Leu	Gly	Asn	Gln	Tyr	His	Leu	Trp	Leu	
			280					285					290			
gag	atg	ctt	gca	cac	act	cca	ttt	tgg	aaa	gac	ttc	act	ctg	gaa	atg	969
Glu	Met	Leu	Ala	His	Thr	Pro	Phe	Trp	Lys	Asp	Phe	Thr	Leu	Glu	Met	
			295				300					305				
caa	aaa	aaa	cgc	ata	gaa	tac	cga	gat	att	gct	caa	aaa	atc	cat	tat	1017
Gln	Lys	Lys	Arg	Ile	Glu	Tyr	Arg	Asp	Ile	Ala	Gln	Lys	Ile	His	Tyr	
			310			315					320					
ttt	tct	caa	gat	aag	cgt	ctt	tat	gaa	gtg	agc	ata	cgc	tcc	att	aag	1065
Phe	Ser	Gln	Asp	Lys	Arg	Leu	Tyr	Glu	Val	Ser	Ile	Arg	Ser	Ile	Lys	
					330					335					340	



340 345 350  
 Glu Arg Trp Ser Lys Pro Ile Lys Thr Phe Phe Gln Lys Asn Phe Phe  
 355 360 365  
 Gln Lys Lys Phe  
 370

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 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
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 taaagagtga aagcggtttt aggagcggtt gagtttcaag agaatgaata tgaagagctt 120  
 aaagagcttt atgagagctt aaaaaaccaag caaaagcccc acactttgtt cattttcttgt 180  
 gtggattcac gagtcgtgcc taattttaatc actggcacca aaccgggcga attgtatgtg 240  
 atttgcaac atg ggc aat gtg aac ccc cct aaa aca agc tat aaa gag tcc 291  
 Met Gly Asn Val Asn Pro Pro Lys Thr Ser Tyr Lys Glu Ser  
 1 5 10  
  
 ctt tct acc att gcg agc att gaa tac gct atc gcg cat gtg ggc gtt 339  
 Leu Ser Thr Ile Ala Ser Ile Glu Tyr Ala Ile Ala His Val Gly Val  
 15 20 25 30  
  
 caa aac tta atc att tgc ggg cat agc gat tgt ggg gct tgc ggg agc 387  
 Gln Asn Leu Ile Ile Cys Gly His Ser Asp Cys Gly Ala Cys Gly Ser  
 35 40 45  
  
 gtt cat tta atc cat gat gaa acc acc aaa gct aaa acc cct tac att 435  
 Val His Leu Ile His Asp Glu Thr Thr Lys Ala Lys Thr Pro Tyr Ile  
 50 55 60  
  
 gca aac tgg ata caa ttt tta gag cct gtt aaa gaa gag tta aaa aac 483  
 Ala Asn Trp Ile Gln Phe Leu Glu Pro Val Lys Glu Glu Leu Lys Asn  
 65 70 75  
  
 cac ccg caa ttc agc aac cat ttc gcc aag cgt tca tgg ctt aca gag 531  
 His Pro Gln Phe Ser Asn His Phe Ala Lys Arg Ser Trp Leu Thr Glu  
 80 85 90  
  
 cgt ttg aat gcg cgc ttg caa ctc aac aac ctc tta agc tat gat ttc 579  
 Arg Leu Asn Ala Arg Leu Gln Leu Asn Asn Leu Leu Ser Tyr Asp Phe  
 95 100 105 110  
  
 att caa gag aaa gcg agc aag aat gaa tta aaa att ttt ggt tgg cac 627  
 Ile Gln Glu Lys Ala Ser Lys Asn Glu Leu Lys Ile Phe Gly Trp His  
 115 120 125  
  
 tac atc ata gaa aca ggc agg att tat aat tat aat ttt gaa agc cat 675  
 Tyr Ile Ile Glu Thr Gly Arg Ile Tyr Asn Tyr Asn Phe Glu Ser His  
 130 135 140  
  
 ttt ttt gag ccg att gga gaa acc att aaa caa agg aaa agt cat gaa 723  
 Phe Phe Glu Pro Ile Gly Glu Thr Ile Lys Gln Arg Lys Ser His Glu  
 145 150 155



aac ttc taaaacaaaa acccctaaat ccgttttaat cgctgggcca tgcgtcattg 779  
 Asn Phe  
 160

a 780

<210> 230  
 <211> 160  
 <212> PRT  
 <213> Helicobacter pylori

<400> 230  
 Met Gly Asn Val Asn Pro Pro Lys Thr Ser Tyr Lys Glu Ser Leu Ser  
 1 5 10 15  
 Thr Ile Ala Ser Ile Glu Tyr Ala Ile Ala His Val Gly Val Gln Asn  
 20 25 30  
 Leu Ile Ile Cys Gly His Ser Asp Cys Gly Ala Cys Gly Ser Val His  
 35 40 45  
 Leu Ile His Asp Glu Thr Thr Lys Ala Lys Thr Pro Tyr Ile Ala Asn  
 50 55 60  
 Trp Ile Gln Phe Leu Glu Pro Val Lys Glu Glu Leu Lys Asn His Pro  
 65 70 75 80  
 Gln Phe Ser Asn His Phe Ala Lys Arg Ser Trp Leu Thr Glu Arg Leu  
 85 90 95  
 Asn Ala Arg Leu Gln Leu Asn Asn Leu Leu Ser Tyr Asp Phe Ile Gln  
 100 105 110  
 Glu Lys Ala Ser Lys Asn Glu Leu Lys Ile Phe Gly Trp His Tyr Ile  
 115 120 125  
 Ile Glu Thr Gly Arg Ile Tyr Asn Tyr Asn Phe Glu Ser His Phe Phe  
 130 135 140  
 Glu Pro Ile Gly Glu Thr Ile Lys Gln Arg Lys Ser His Glu Asn Phe  
 145 150 155 160

<210> 231  
 <211> 450  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (107)...(385)

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 taataaaagac ttataaaagt aattaaaaatt aaacagaagg gtttttg atg tcc gct 115  
 Met Ser Ala  
 1  
 cat ttt tta aaa atc gtt ttt tta gta ggc atg tgc gtt tca agt ttg 163  
 His Phe Leu Lys Ile Val Phe Leu Val Gly Met Cys Val Ser Ser Leu  
 5 10 15  
 ttc gct gaa ggt tta gag ggg ttt ttt aac gcc cta gaa gcc cag ctc 211  
 Phe Ala Glu Gly Leu Glu Gly Phe Phe Asn Ala Leu Glu Ala Gln Leu  
 20 25 30 35  
 aaa agc ccc atc gct aag ggg att tta atg gtg att ttc ata ggg atc 259  
 Lys Ser Pro Ile Ala Lys Gly Ile Leu Met Val Ile Phe Ile Gly Ile





cta gac gct tct ttt agc gct cac atg ccc gat tgc tta gaa atg cct	976
Leu Asp Ala Ser Phe Ser Ala His Met Pro Asp Cys Leu Glu Met Pro	
285 290 295 300	
tat cgc cct agc att ttt aaa gtc tcc gta gaa aat gat gaa gag ctt	1024
Tyr Arg Pro Ser Ile Phe Lys Val Ser Val Glu Asn Asp Glu Glu Leu	
305 310 315	
att gaa gtt gaa aag ggc gaa aat caa ggg gcg ttt tct tat ttt tta	1072
Ile Glu Val Glu Lys Gly Glu Asn Gln Gly Ala Phe Ser Tyr Phe Leu	
320 325 330	
ggc ggc cct act tgt tta gcg ggg gat ttt atg ggg agt ttt agc ttt	1120
Gly Gly Pro Thr Cys Leu Ala Gly Asp Phe Met Gly Ser Phe Ser Phe	
335 340 345	
gaa acg cct tta aaa agg ggc gat aaa atc gtg ttt caa gac atg ctc	1168
Glu Thr Pro Leu Lys Arg Gly Asp Lys Ile Val Phe Gln Asp Met Leu	
350 355 360	
cat tat acg att gtc aaa aac aac tcg ttt aat ggc gtg ccg ctc cca	1216
His Tyr Thr Ile Val Lys Asn Asn Ser Phe Asn Gly Val Pro Leu Pro	
365 370 375 380	
agc ctg gct aga ttg gat caa caa ggg ttt aaa atc ctt aaa aac ttt	1264
Ser Leu Ala Arg Leu Asp Gln Gln Gly Phe Lys Ile Leu Lys Asn Phe	
385 390 395	
tct tat gaa gac tat aaa aac aga aac taaagctttt gattaaggct	1311
Ser Tyr Glu Asp Tyr Lys Asn Arg Asn	
400 405	
ttttggggct tgtaaaaaagt tacgcacaac attccaac	1349
<210> 234	
<211> 405	
<212> PRT	
<213> Helicobacter pylori	
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Glu Arg Leu Glu Lys Asn Ala Lys Ile Leu Glu Ile Val Arg Gln Gln	
20 25 30	
Ser Gly Ala Lys Val Leu Leu Ala Leu Lys Gly Tyr Ala Phe Trp Arg	
35 40 45	
Glu Phe Gly Ile Leu Arg Gln Lys Leu Asn Gly Cys Cys Ala Ser Gly	
50 55 60	
Leu Tyr Glu Ala Lys Leu Ala Phe Glu Glu Phe Gly Gly Arg Glu Ser	
65 70 75 80	
His Lys Glu Ile Cys Val Tyr Ser Pro Ala Phe Lys Glu Ala Glu Met	
85 90 95	
Ser Ala Ile Leu Pro Leu Ala Thr Ser Ile Ile Phe Asn Ser Phe Tyr	
100 105 110	
Gln Tyr Ala Thr Tyr Lys Asp Arg Ile Leu Asp Lys Asn Lys Gln Leu	
115 120 125	
Glu Asn Leu Gly Leu Ser Pro Ile Lys Met Gly Leu Arg Ile Asn Pro	
130 135 140	
Leu Tyr Ser Glu Val Thr Pro Ala Ile Tyr Asn Pro Cys Ser Lys Val	

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145	Ser Arg Leu Gly Ile	150	Thr Pro Ser Gly Phe	155	Glu Lys Gly Val Lys	160	Glu
	165	Val Ser Gly Leu His	170	Phe His Thr His Cys	175	Glu	
His Gly Leu Glu Gly	180	Val Ser Gly Leu His	185	Phe His Thr His Cys	190	Glu	
Gln Asn Ala Asp Ala	195	Leu Cys Arg Thr Leu	200	Glu His Val Glu Lys	205	His	
Phe Arg Pro Tyr Leu	210	Glu Asn Met Ala Trp	215	Val Asn Phe Gly Gly	220	Gly	
His His Ile Thr Lys	225	Ser Asp Tyr Asp Val	230	Asn Leu Leu Ile Gln	235	Thr	
Ile Lys Asp Phe Lys	245	Glu Arg Tyr His Asn	250	Ile Glu Val Ile Leu	255	Glu	
Pro Gly Glu Ala Ile	260	Gly Trp Gln Cys Gly	265	Phe Leu Ile Ala Ser	270	Val	
Ile Asp Ile Val Gln	275	Asn Asp Gln Glu Ile	280	Ala Ile Leu Asp Ala	285	Ser	
Phe Ser Ala His Met	290	Pro Asp Cys Leu Glu	295	Met Pro Tyr Arg Pro	300	Ser	
Ile Phe Lys Val Ser	305	Val Glu Asn Asp Glu	310	Glu Leu Ile Glu Val	315	Glu	
Lys Gly Glu Asn Gln	325	Gly Ala Phe Ser Tyr	330	Phe Leu Gly Gly Pro	335	Thr	
Cys Leu Ala Gly Asp	340	Phe Met Gly Ser Phe	345	Ser Phe Glu Thr Pro	350	Leu	
Lys Arg Gly Asp Lys	355	Ile Val Phe Gln Asp	360	Met Leu His Tyr Thr	365	Ile	
Val Lys Asn Asn Ser	370	Phe Asn Gly Val Pro	375	Leu Pro Ser Leu Ala	380	Arg	
Leu Asp Gln Gln Gly	385	Phe Lys Ile Leu Lys	390	Asn Phe Ser Tyr Glu	395	Asp	
Tyr Lys Asn Arg Asn	405						

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 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (246)...(548)

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ctcatctttac acttgcaggc tcgcatggcc caaactacga caacaaagtg ccttttaaatt	120
ttaggggtggt taagccttat tgctcaagcg ctgatctgtc ttcttgctcc aaagaaagcc	180
tgattaacgc ctatgacaac accatttttt acaacgacta tctgctagat cgaaagatca	240
ttagc atg ctt gaa aac gcc aag cag ccc gcc tta atg atc tat tta agc	290
Met Leu Glu Asn Ala Lys Gln Pro Ala Leu Met Ile Tyr Leu Ser	
1 5 10 15	
gat cat ggc gaa agt ttg ggc gaa gaa gcg ttc tat ttg cat ggc att	338
Asp His Gly Glu Ser Leu Gly Glu Glu Ala Phe Tyr Leu His Gly Ile	
20 25 30	
cct aaa agc atc gcc ccc aaa gaa caa tac gag atc ccc ttt atc gtt	386
Pro Lys Ser Ile Ala Pro Lys Glu Gln Tyr Glu Ile Pro Phe Ile Val	
35 40 45	



tat aac att tcg gtt aaa aac aat ttt ccc acc cta aag agc gct aaa	263
Tyr Asn Ile Ser Val Lys Asn Asn Phe Pro Thr Leu Lys Ser Ala Lys	
35 40 45	
agg caa ggc ata gat ttt ggg gaa tgg gat aaa aat ttc aag ctt tta	311
Arg Gln Gly Ile Asp Phe Gly Glu Trp Asp Lys Asn Phe Lys Leu Leu	
50 55 60	
gaa tgg atc gca cgc tac gcc ccc tta gtc aat cca aac ggc tgc atg	359
Glu Trp Ile Ala Arg Tyr Ala Pro Leu Val Asn Pro Asn Gly Cys Met	
65 70 75	
gtt att ttt tgc tct tac agg ttt ata agc tat atc gct gat ttt tta	407
Val Ile Phe Cys Ser Tyr Arg Phe Ile Ser Tyr Ile Ala Asp Phe Leu	
80 85 90 95	
gaa gaa aac ggc ttt gtg gtc aaa gac ttt atc caa tgg gtt aaa aat	455
Glu Glu Asn Gly Phe Val Val Lys Asp Phe Ile Gln Trp Val Lys Asn	
100 105 110	
aat ccc atg cca aga aac att cac cgg cgt tat gtc caa gac acg gaa	503
Asn Pro Met Pro Arg Asn Ile His Arg Arg Tyr Val Gln Asp Thr Glu	
115 120 125	
ttt gct ctg tgg gcg gtt aaa aag aaa gcc aag tgg gtg ttt aac aaa	551
Phe Ala Leu Trp Ala Val Lys Lys Lys Ala Lys Trp Val Phe Asn Lys	
130 135 140	
ccc aaa aat gaa aaa tat tta cgg cct ttg att tta aaa agc cct gtg	599
Pro Lys Asn Glu Lys Tyr Leu Arg Pro Leu Ile Leu Lys Ser Pro Val	
145 150 155	
gta agc ggg ctt gaa aaa acc aaa cac ccc acg caa aaa agc ctg gcc	647
Val Ser Gly Leu Glu Lys Thr Lys His Pro Thr Gln Lys Ser Leu Ala	
160 165 170 175	
tta atg gaa aaa atc att tcc atc cac aca aac cct aat gac atc gtg	695
Leu Met Glu Lys Ile Ile Ser Ile His Thr Asn Pro Asn Asp Ile Val	
180 185 190	
cta gat cct ttc atg ggg agc ggc acc acc ggc tta gcg tgc aaa aat	743
Leu Asp Pro Phe Met Gly Ser Gly Thr Thr Gly Leu Ala Cys Lys Asn	
195 200 205	
tta gaa cgg aat ttt atc ggc ata gaa tca gaa aaa gaa tat ttt caa	791
Leu Glu Arg Asn Phe Ile Gly Ile Glu Ser Glu Lys Glu Tyr Phe Gln	
210 215 220	
acc gct aaa aag cgt ttg aat ctg ttt taaaaacgct atttgaatga	838
Thr Ala Lys Lys Arg Leu Asn Leu Phe	
225 230	
gattgtgtta tagttattta aaaggatatt ttga	872

<210> 238  
 <211> 232  
 <212> PRT  
 <213> Helicobacter pylori

<400> 238  
 Met Ile Gln Ile Tyr His Ala Asp Ala Phe Glu Ile Ile Lys Asp Phe  
 1 5 10 15  
 Tyr Gln Gln Asn Leu Lys Val Asp Ala Ile Ile Thr Asp Pro Pro Tyr  
 20 25 30  
 Asn Ile Ser Val Lys Asn Asn Phe Pro Thr Leu Lys Ser Ala Lys Arg  
 35 40 45  
 Gln Gly Ile Asp Phe Gly Glu Trp Asp Lys Asn Phe Lys Leu Leu Glu  
 50 55 60  
 Trp Ile Ala Arg Tyr Ala Pro Leu Val Asn Pro Asn Gly Cys Met Val  
 65 70 75 80  
 Ile Phe Cys Ser Tyr Arg Phe Ile Ser Tyr Ile Ala Asp Phe Leu Glu  
 85 90 95  
 Glu Asn Gly Phe Val Val Lys Asp Phe Ile Gln Trp Val Lys Asn Asn  
 100 105 110  
 Pro Met Pro Arg Asn Ile His Arg Arg Tyr Val Gln Asp Thr Glu Phe  
 115 120 125  
 Ala Leu Trp Ala Val Lys Lys Lys Ala Lys Trp Val Phe Asn Lys Pro  
 130 135 140  
 Lys Asn Glu Lys Tyr Leu Arg Pro Leu Ile Leu Lys Ser Pro Val Val  
 145 150 155 160  
 Ser Gly Leu Glu Lys Thr Lys His Pro Thr Gln Lys Ser Leu Ala Leu  
 165 170 175  
 Met Glu Lys Ile Ile Ser Ile His Thr Asn Pro Asn Asp Ile Val Leu  
 180 185 190  
 Asp Pro Phe Met Gly Ser Gly Thr Thr Gly Leu Ala Cys Lys Asn Leu  
 195 200 205  
 Glu Arg Asn Phe Ile Gly Ile Glu Ser Glu Lys Glu Tyr Phe Gln Thr  
 210 215 220  
 Ala Lys Lys Arg Leu Asn Leu Phe  
 225 230

<210> 239  
 <211> 1181  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (60)...(1124)

<400> 239  
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 atg aat tat aaa att tta gat tta ttt tgt ggg gct ggg ggt ttt agc 107  
 Met Asn Tyr Lys Ile Leu Asp Leu Phe Cys Gly Ala Gly Gly Phe Ser  
 1 5 10 15  
 gct ggg tta gag tgt tta gaa gag ttt gac gct tta ata ggg cta gat 155  
 Ala Gly Leu Glu Cys Leu Glu Glu Phe Asp Ala Leu Ile Gly Leu Asp  
 20 25 30  
 tgc gat aaa caa gcc cta atc act ttt gaa aac aac cat aaa aac gcc 203  
 Cys Asp Lys Gln Ala Leu Ile Thr Phe Glu Asn Asn His Lys Asn Ala  
 35 40 45  
 ata ggc gtt tgt ggg gac atc act caa acc gaa att aaa gaa aaa gtc 251  
 Ile Gly Val Cys Gly Asp Ile Thr Gln Thr Glu Ile Lys Glu Lys Val  
 50 55 60



atc Ile 65	aaa Lys	cta Leu	gct Ala	aaa Lys	aaa Lys 70	tta Leu	gaa Glu	atc Ile	aac Asn	atg Met 75	atc Ile	att Ile	ggc Gly	ggg Gly	cct Pro 80	299
cca Pro	tgt Cys	caa Gln	ggc Gly	ttt Phe 85	tct Ser	aat Asn	aaa Lys	ggg Gly	aaa Lys 90	aat Asn	tta Leu	ggg Gly	cta Leu	aaa Lys 95	gac Asp	347
cct Pro	agg Arg	aat Asn	ttt Phe 100	tta Leu	ttc Phe	tta Leu	gaa Glu	tat Tyr 105	ata Ile	gaa Glu	ata Ile	gtc Val	aaa Lys 110	gcc Ala	ata Ile	395
aag Lys	cca Pro	gaa Glu 115	att Ile	ttt Phe	atc Ile	att Ile	gaa Glu 120	aac Asn	gtg Val	aaa Lys	aac Asn	ctc Leu 125	atc Ile	tct Ser	tgc Cys	443
gct Ala	aaa Lys 130	ggc Gly	tat Tyr	ttt Phe	tta Leu	gaa Glu 135	gaa Glu	att Ile	aaa Lys	gaa Glu	agg Arg 140	ttg Leu	aac Asn	gct Ala	tta Leu	491
ggg Gly 145	tat Tyr	caa Gln	ttg Leu	agc Ser 150	tat Tyr	caa Gln	atc Ile	cta Leu	aac Asn	gct Ala 155	aaa Lys	gat Asp	tat Tyr	ggc Gly	gtg Val 160	539
cct Pro	caa Gln	aac Asn	aga Arg 165	gag Glu	aga Arg	gcc Ala	ttt Phe	att Ile	gta Val 170	ggg Gly	gct Ala	agt Ser	cgt Arg	ttc Phe 175	agt Ser	587
ttt Phe	gat Asp	ttc Phe	aat Asn 180	ctt Leu	tta Leu	gag Glu	cct Pro	tct Ser 185	caa Gln	agc Ser	gtg Val	aat Asn	gtt Val 190	caa Gln	gat Asp	635
gcc Ala	ata Ile	agc Ser 195	gat Asp	tta Leu	gcc Ala	tat Tyr 200	ctt Leu	tgt Cys	tct Ser	aat Asn	gag Glu	ggg Gly 205	gcg Ala	ttt Phe	gag Glu	683
agc Ser	gat Asp 210	tat Tyr	tta Leu	aac Asn	cct Pro	atc Ile 215	caa Gln	tca Ser	agc Ser	tat Tyr	caa Gln 220	gct Ala	tta Leu	atg Met	cga Arg	731
aaa Lys 225	gat Asp	agc Ser	cct Pro	aaa Lys	tta Leu 230	tac Tyr	aac Asn	cat His	caa Gln	gcc Ala 235	acc Thr	aac Asn	cac His	tcg Ser	caa Gln 240	779
gcc Ala	gct Ala	tta Leu	gag Glu	aaa Lys 245	tta Leu	aaa Lys	ctc Leu	att Ile	aac Asn 250	aaa Lys	gaa Glu	caa Gln	ggc Gly	aaa Lys 255	gaa Glu	827
tgc Cys	ttg Leu	cct Pro	aaa Lys 260	aac Asn	ttg Leu	cat His	ggc Gly	aaa Lys 265	cag Gln	caa Gln	ttc Phe	aaa Lys	agc Ser 270	aca Thr	tgg Trp	875
ggg Gly	cgc Arg	ctg Leu 275	aat Asn	tgg Trp	aat Asn	aaa Lys	atc Ile 280	agc Ser	ccc Pro	acc Thr	ata Ile	gac Asp 285	aca Thr	cga Arg	ttt Phe	923
gac Asp	act Thr 290	ccc Pro	agc Ser	aat Asn	ggc Gly	acc Thr 295	aac Asn	tcc Ser	cac His	ccc Pro	gaa Glu 300	ttg Leu	cac His	cgc Arg	tct Ser	971

atc acg cct aga gaa gcc gct agg ata caa agt ttt agc gat aat tat 1019  
 Ile Thr Pro Arg Glu Ala Ala Arg Ile Gln Ser Phe Ser Asp Asn Tyr  
 305 310 315 320

atc ttt tat ggc aat aaa acg agc gtt tgt aag caa atc ggt aac gct 1067  
 Ile Phe Tyr Gly Asn Lys Thr Ser Val Cys Lys Gln Ile Gly Asn Ala  
 325 330 335

gtg cct cct ctt cta gcc cta gcc tta ggc aaa gcg atc tta aaa agc 1115  
 Val Pro Pro Leu Leu Ala Leu Ala Leu Gly Lys Ala Ile Leu Lys Ser  
 340 345 350

tta aga aaa tgatacaaat ttatcacgct gacgcttttg aaatcatcaa 1164  
 Leu Arg Lys  
 355

agactttttac cagcaaa 1181

<210> 240  
 <211> 355  
 <212> PRT  
 <213> Helicobacter pylori

<400> 240  
 Met Asn Tyr Lys Ile Leu Asp Leu Phe Cys Gly Ala Gly Gly Phe Ser  
 1 5 10 15  
 Ala Gly Leu Glu Cys Leu Glu Glu Phe Asp Ala Leu Ile Gly Leu Asp  
 20 25 30  
 Cys Asp Lys Gln Ala Leu Ile Thr Phe Glu Asn Asn His Lys Asn Ala  
 35 40 45  
 Ile Gly Val Cys Gly Asp Ile Thr Gln Thr Glu Ile Lys Glu Lys Val  
 50 55 60  
 Ile Lys Leu Ala Lys Lys Leu Glu Ile Asn Met Ile Ile Gly Gly Pro  
 65 70 75 80  
 Pro Cys Gln Gly Phe Ser Asn Lys Gly Lys Asn Leu Gly Leu Lys Asp  
 85 90 95  
 Pro Arg Asn Phe Leu Phe Leu Glu Tyr Ile Glu Ile Val Lys Ala Ile  
 100 105 110  
 Lys Pro Glu Ile Phe Ile Ile Glu Asn Val Lys Asn Leu Ile Ser Cys  
 115 120 125  
 Ala Lys Gly Tyr Phe Leu Glu Glu Ile Lys Glu Arg Leu Asn Ala Leu  
 130 135 140  
 Gly Tyr Gln Leu Ser Tyr Gln Ile Leu Asn Ala Lys Asp Tyr Gly Val  
 145 150 155 160  
 Pro Gln Asn Arg Glu Arg Ala Phe Ile Val Gly Ala Ser Arg Phe Ser  
 165 170 175  
 Phe Asp Phe Asn Leu Leu Glu Pro Ser Gln Ser Val Asn Val Gln Asp  
 180 185 190  
 Ala Ile Ser Asp Leu Ala Tyr Leu Cys Ser Asn Glu Gly Ala Phe Glu  
 195 200 205  
 Ser Asp Tyr Leu Asn Pro Ile Gln Ser Ser Tyr Gln Ala Leu Met Arg  
 210 215 220  
 Lys Asp Ser Pro Lys Leu Tyr Asn His Gln Ala Thr Asn His Ser Gln  
 225 230 235 240  
 Ala Ala Leu Glu Lys Leu Lys Leu Ile Asn Lys Glu Gln Gly Lys Glu  
 245 250 255  
 Cys Leu Pro Lys Asn Leu His Gly Lys Gln Gln Phe Lys Ser Thr Trp  
 260 265 270

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aac Asn	gct Ala	ttg Leu	aaa Lys 135	ttc Phe	ctt Leu	att Ile	tta Leu	tat Tyr 140	att Ile	caa Gln	aag Lys	gta Val	tta Leu 145	atg Met	gat Asp	489
agt Ser	ggg Gly	att Ile 150	tat Tyr	cct Pro	tta Leu	ttt Phe	gac Asp 155	aac Asn	ttt Phe	tta Leu	caa Gln	aaa Lys 160	caa Gln	gac Asp	aca Thr	537
gaa Glu	agt Ser 165	ttt Phe	aag Lys	caa Gln	cta Leu	aaa Lys 170	gat Asp	ggg Gly	ttc Phe	act Thr	cat His 175	ttt Phe	act Thr	atc Ile	aat Asn	585
aac Asn 180	aca Thr	gca Ala	atc Ile	aat Asn	aac Asn 185	gct Ala	acg Thr	gaa Glu	tgt Cys	ttt Phe 190	agg Arg	att Ile	ttt Phe	act Thr	aaa Lys 195	633
att Ile	atc Ile	aat Asn	cct Pro	tta Leu 200	gct Ala	ttt Phe	tat Tyr	tat Tyr	ggg Gly 205	aaa Lys	aaa Lys	ggc Gly	aca Thr	aga Arg 210	aaa Lys	681
ggg Gly	tat Tyr	ttg Leu	tcc Ser 215	aac Asn	act Thr	ata Ile	att Ile	aca Thr 220	aaa Lys	gat Asp	gag Glu	ctt Leu 225	aat Asn	tat Tyr	aat Asn	729
cgt Arg	atc Ile	aat Asn 230	tgg Trp	cga Arg	gat Asp	ata Ile	gga Gly 235	aaa Lys	gat Asp	aaa Lys	aat Asn	acc Thr 240	acc Thr	aga Arg	caa Gln	777
gaa Glu	tac Tyr 245	gat Asp	ctt Leu	ata Ile	aac Asn	tct Ser 250	aaa Lys	agg Arg	att Ile	gct Ala	aat Asn 255	tct Ser	aac Asn	tat Tyr	ctt Leu	825
att Ile 260	tca Ser	aaa Lys	gct Ala	aag Lys	aaa Lys 265	gtg Val	gtg Val	aaa Lys	cga Arg	tat Tyr 270	aat Asn	gat Asp	aga Arg	ttt Phe	aat Asn 275	873
aat Asn	tct Ser	ctc Leu	tct Ser	gaa Glu 280	gta Val	aaa Lys	caa Gln	gaa Glu	aaa Lys 285	gaa Glu	gag Glu	tcg Ser	caa Gln	gcc Ala 290	aca Thr	921
caa Gln	ata Ile	cac His	cat His 295	att Ile	ttt Phe	ccc Pro	atc Ile	caa Gln 300	gac Asp	ttt Phe	ccc Pro	att Ile	att Ile 305	gct Ala	aac Asn	969
tat Tyr	ata Ile	gag Glu 310	aat Asn	ctt Leu	atc Ile	gca Ala	ctc Leu 315	act Thr	cct Pro	aat Asn	caa Gln	cat His 320	ttt Phe	att Ile	tac Tyr	1017
gcc Ala	cac His 325	cct Pro	aat Asn	aat Asn	caa Gln	acc Thr 330	cgc Arg	ttg Leu	att Ile	gat Asp	aaa Lys 335	gat Asp	ttt Phe	caa Gln	tat Tyr	1065
atc Ile 340	tgc Cys	tta Leu	tta Leu	gct Ala	aaa Lys 345	acg Thr	acc Thr	aca Thr	att Ile	ctt Leu 350	aat Asn	gac Asp	act Thr	caa Gln	ggc Gly 355	1113
gta Val	tat Tyr	gat Asp	tgg Trp	aat Asn 360	gat Asp	tat Tyr	att Ile	gtt Val 365	gtg Val	ttg Leu	aat Asn	atg Met	ggc Gly 370	ctc Leu	aaa Lys	1161

aca act atc ttt tct caa gtc aag aac gaa tgg gaa tta tta aaa gta 1209  
 Thr Thr Ile Phe Ser Gln Val Lys Asn Glu Trp Glu Leu Leu Lys Val  
 375 380 385

ata gat gct ttt tat ttt gat ttt aac aag agc aaa gat cca agt tgg 1257  
 Ile Asp Ala Phe Tyr Phe Asp Phe Asn Lys Ser Lys Asp Pro Ser Trp  
 390 395 400

tca tac ttg cta gat aaa aac gat tta aga gct ttc aag cta aaa ttt 1305  
 Ser Tyr Leu Leu Asp Lys Asn Asp Leu Arg Ala Phe Lys Leu Lys Phe  
 405 410 415

taataagttt tattgaaact ggctataaaa acccgcttga cttatcttat cctttt 1361

<210> 242  
 <211> 419  
 <212> PRT  
 <213> Helicobacter pylori

<400> 242  
 Met Lys Glu Gln Ser Met Ile Asp Phe Leu Lys Leu Arg Asp Tyr Asp  
 1 5 10 15  
 Ile Arg Lys Thr Gln Asn Ala Arg Trp Ile Asp Gln Lys Cys Thr Pro  
 20 25 30  
 Asp Val Leu Ser Leu Val Ala Asp Cys Ile Leu Glu Phe Thr Gln Cys  
 35 40 45  
 Asn Ile Gly Lys Ser Phe Ser Ile Arg Asp Ile Trp Asp Ser Pro Tyr  
 50 55 60  
 Thr Asn Glu Asn Val Lys Met Ile Phe Ser Lys Pro Asp Leu Asn Ser  
 65 70 75 80  
 Asp Phe Ser Met His Glu Tyr Asp Lys Phe Phe Ser Gln Pro Ile Lys  
 85 90 95  
 Leu Leu Ala Tyr Ser Gly Ile Leu Phe Glu Thr Lys Thr Gly Asn Arg  
 100 105 110  
 Asn Ile Tyr Thr Ile Gln Asn Ile Glu Leu Leu Glu Tyr Leu Met Gln  
 115 120 125  
 Arg Glu Thr Asn Ala Leu Lys Phe Leu Ile Leu Tyr Ile Gln Lys Val  
 130 135 140  
 Leu Met Asp Ser Gly Ile Tyr Pro Leu Phe Asp Asn Phe Leu Gln Lys  
 145 150 155 160  
 Gln Asp Thr Glu Ser Phe Lys Gln Leu Lys Asp Gly Phe Thr His Phe  
 165 170 175  
 Thr Ile Asn Asn Thr Ala Ile Asn Asn Ala Thr Glu Cys Phe Arg Ile  
 180 185 190  
 Phe Thr Lys Ile Ile Asn Pro Leu Ala Phe Tyr Tyr Gly Lys Lys Gly  
 195 200 205  
 Thr Arg Lys Gly Tyr Leu Ser Asn Thr Ile Ile Thr Lys Asp Glu Leu  
 210 215 220  
 Asn Tyr Asn Arg Ile Asn Trp Arg Asp Ile Gly Lys Asp Lys Asn Thr  
 225 230 235 240  
 Thr Arg Gln Glu Tyr Asp Leu Ile Asn Ser Lys Arg Ile Ala Asn Ser  
 245 250 255  
 Asn Tyr Leu Ile Ser Lys Ala Lys Lys Val Val Lys Arg Tyr Asn Asp  
 260 265 270  
 Arg Phe Asn Asn Ser Leu Ser Glu Val Lys Gln Glu Lys Glu Glu Ser  
 275 280 285  
 Gln Ala Thr Gln Ile His His Ile Phe Pro Ile Gln Asp Phe Pro Ile  
 290 295 300

09895913-062901

Ile Ala Asn Tyr Ile Glu Asn Leu Ile Ala Leu Thr Pro Asn Gln His  
 305 310 315 320  
 Phe Ile Tyr Ala His Pro Asn Asn Gln Thr Arg Leu Ile Asp Lys Asp  
 325 330 335  
 Phe Gln Tyr Ile Cys Leu Leu Ala Lys Thr Thr Thr Ile Leu Asn Asp  
 340 345 350  
 Thr Gln Gly Val Tyr Asp Trp Asn Asp Tyr Ile Val Val Leu Asn Met  
 355 360 365  
 Gly Leu Lys Thr Thr Ile Phe Ser Gln Val Lys Asn Glu Trp Glu Leu  
 370 375 380  
 Leu Lys Val Ile Asp Ala Phe Tyr Phe Asp Phe Asn Lys Ser Lys Asp  
 385 390 395 400  
 Pro Ser Trp Ser Tyr Leu Leu Asp Lys Asn Asp Leu Arg Ala Phe Lys  
 405 410 415  
 Leu Lys Phe

<210> 243  
 <211> 2610  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (90)...(2558)

<400> 243  
 taaagaggct tttgaaacca tgcttaaaga aattgagagc ttgaaacatt aatgcttcaa 60  
 atgaatttgg tttaatcctt aatccccctt atg ctc ttt gat caa acc tta acc 113  
 Met Leu Phe Asp Gln Thr Leu Thr  
 1 5  
 tat att tct tta ttt tct ggg gca gga gtg ggg tgc tat ggg ctt tta 161  
 Tyr Ile Ser Leu Phe Ser Gly Ala Gly Val Gly Cys Tyr Gly Leu Leu  
 10 15 20  
 gaa gag ggg ttt gaa tgc gtt gct acc aat gaa att tta gaa aaa cgc 209  
 Glu Glu Gly Phe Glu Cys Val Ala Thr Asn Glu Ile Leu Glu Lys Arg  
 25 30 35 40  
 ttg aat atc caa agg att aat cgc aaa tgc aaa tta gat gaa agc tac 257  
 Leu Asn Ile Gln Arg Ile Asn Arg Lys Cys Lys Leu Asp Glu Ser Tyr  
 45 50 55  
 att agt ggg gac att aaa aag cca gaa aca aaa gaa aaa att tta aag 305  
 Ile Ser Gly Asp Ile Lys Lys Pro Glu Thr Lys Glu Lys Ile Leu Lys  
 60 65 70  
 caa att gaa ttt tat tct aaa aaa ttt ggt aat gat agg gtt gat tta 353  
 Gln Ile Glu Phe Tyr Ser Lys Lys Phe Gly Asn Asp Arg Val Asp Leu  
 75 80 85  
 gtg gta gca acc cca cct tgt caa ggc atg agc gta gcc aat cat aag 401  
 Val Val Ala Thr Pro Pro Cys Gln Gly Met Ser Val Ala Asn His Lys  
 90 95 100  
 aag aaa aac gat gag atc aaa cgg aat tct ttg gtg gtt gaa agc att 449  
 Lys Lys Asn Asp Glu Ile Lys Arg Asn Ser Leu Val Val Glu Ser Ile  
 105 110 115 120

gat ttg atc aaa caa atc aaa ccc aga ttt ttt att tta gaa aat gtc Asp Leu Ile Lys Gln Ile Lys Pro Arg Phe Phe Ile Leu Glu Asn Val 125 130 135	497
cct agt ttt tat aaa aca ggt tgt ata gac aaa aat gat aat ttg cta Pro Ser Phe Tyr Lys Thr Gly Cys Ile Asp Lys Asn Asp Asn Leu Leu 140 145 150	545
gaa ata gga tct atg ata gag caa aat ttg agt ggc gat tat atg ctc Glu Ile Gly Ser Met Ile Glu Gln Asn Leu Ser Gly Asp Tyr Met Leu 155 160 165	593
tat gat gag gta atc aat ttt aaa aat ttt gga gct aat tca agc cga Tyr Asp Glu Val Ile Asn Phe Lys Asn Phe Gly Ala Asn Ser Ser Arg 170 175 180	641
aca aga act tta gtg ata ggg gtt tgt aaa gag ttt aaa gat ttt ata Thr Arg Thr Leu Val Ile Gly Val Cys Lys Glu Phe Lys Asp Phe Ile 185 190 195 200	689
agc gcg tta gaa ttt ttt cct gat ttc aaa caa gaa aaa acc tta aaa Ser Ala Leu Glu Phe Phe Pro Asp Phe Lys Gln Glu Lys Thr Leu Lys 205 210 215	737
gaa gtg ata gga tcg tta aaa cca ctt gct tgg ggc gag tat gac aac Glu Val Ile Gly Ser Leu Lys Pro Leu Ala Trp Gly Glu Tyr Asp Asn 220 225 230	785
acg gat ttt tat cat agt ttt aga act tat cca aag cat atg caa gaa Thr Asp Phe Tyr His Ser Phe Arg Thr Tyr Pro Lys His Met Gln Glu 235 240 245	833
tgg att aag gat tta aaa gaa gga caa agc gcg ttt gag aat aca gaa Trp Ile Lys Asp Leu Lys Glu Gly Gln Ser Ala Phe Glu Asn Thr Glu 250 255 260	881
tta aac aaa aaa cct cat aga att gtt ggc agt aag att gtc tta aat Leu Asn Lys Lys Pro His Arg Ile Val Gly Ser Lys Ile Val Leu Asn 265 270 275 280	929
gtt tct aaa aat ggc gat aaa tat aaa aga caa aaa tat cat agc gtt Val Ser Lys Asn Gly Asp Lys Tyr Lys Arg Gln Lys Tyr His Ser Val 285 290 295	977
gcc cct tgc att cat aca aga aac gac caa atg gct agc caa aac acg Ala Pro Cys Ile His Thr Arg Asn Asp Gln Met Ala Ser Gln Asn Thr 300 305 310	1025
atc cac ccc aaa gat gat aga gtg ttt tcc att aga gag ctg atg ctt Ile His Pro Lys Asp Asp Arg Val Phe Ser Ile Arg Glu Leu Met Leu 315 320 325	1073
tta atg aat atc cct agc cgt ttt aag tgg tta gat tta gaa tta caa Leu Met Asn Ile Pro Ser Arg Phe Lys Trp Leu Asp Leu Glu Leu Gln 330 335 340	1121
gaa tta aac gcc ctt aac caa caa gaa aaa gaa aaa atc tcc aaa caa Glu Leu Asn Ala Leu Asn Gln Gln Glu Lys Glu Lys Ile Ser Lys Gln	1169

345	350	355	360	
aac gaa atg aat ata aga caa agc atc ggt gaa gct gtt cca acg att				1217
Asn Glu Met Asn Ile Arg Gln Ser Ile Gly Glu Ala Val Pro Thr Ile	365	370	375	
att ttt aag caa att gcc ata aag ata aaa aat ttc atg tct caa acc				1265
Ile Phe Lys Gln Ile Ala Ile Lys Ile Lys Asn Phe Met Ser Gln Thr	380	385	390	
cac tta gag cct aaa gaa atc att agg ctt att gat gtg cac cat tta				1313
His Leu Glu Pro Lys Glu Ile Ile Arg Leu Ile Asp Val His His Leu	395	400	405	
tta gag cca caa aat ttg aag cga ttt att tta gaa aat caa aac aag				1361
Leu Glu Pro Gln Asn Leu Lys Arg Phe Ile Leu Glu Asn Gln Asn Lys	410	415	420	
att gca aga gcg agt tta gtg agt ttg gca gaa atg tct aat tct aaa				1409
Ile Ala Arg Ala Ser Leu Val Ser Leu Ala Glu Met Ser Asn Ser Lys	425	430	435	440
cgc ata gaa aaa agc gcg tat ttt aca aac cct ttt att att aat gaa				1457
Arg Ile Glu Lys Ser Ala Tyr Phe Thr Asn Pro Phe Ile Ile Asn Glu	445	450	455	
ata gcg aag tta ttg cca agc ttt aaa caa gag agt gtt act att ata				1505
Ile Ala Lys Leu Leu Pro Ser Phe Lys Gln Glu Ser Val Thr Ile Ile	460	465	470	
gag cca agt gca ggg tgt ggg aat ttc tta agt gct ctt ttt aaa aaa				1553
Glu Pro Ser Ala Gly Cys Gly Asn Phe Leu Ser Ala Leu Phe Lys Lys	475	480	485	
tac act tct gtt aaa aaa gtt tat tta aag tgt ata gat att gat aaa				1601
Tyr Thr Ser Val Lys Lys Val Tyr Leu Lys Cys Ile Asp Ile Asp Lys	490	495	500	
aat agt tta gaa att tta gag att tta tat aaa gat tgc att cct aac				1649
Asn Ser Leu Glu Ile Leu Glu Ile Leu Tyr Lys Asp Cys Ile Pro Asn	505	510	515	520
aat ttt gag atg gaa ttg att tgc aaa gat ttt cta gcc tat gaa tgc				1697
Asn Phe Glu Met Glu Leu Ile Cys Lys Asp Phe Leu Ala Tyr Glu Cys	525	530	535	
ggc aaa gtg gat tta att gtg ggc aat ccg cct ttt ggc aaa acg cat				1745
Gly Lys Val Asp Leu Ile Val Gly Asn Pro Pro Phe Gly Lys Thr His	540	545	550	
gaa aga ttc aaa gat tat agt tta aga ctc act cat tta gca ggg att				1793
Glu Arg Phe Lys Asp Tyr Ser Leu Arg Leu Thr His Leu Ala Gly Ile	555	560	565	
ttt tta gaa aag tct tta aaa cta gcc aac ttt aca gcg atg gtt atg				1841
Phe Leu Glu Lys Ser Leu Lys Leu Ala Asn Phe Thr Ala Met Val Met	570	575	580	
cct aaa aac ctt tta aac act aaa gag tat gca gaa act aga act aag				1889



Pro Lys Asn Leu Leu Asn Thr Lys Glu Tyr Ala Glu Thr Arg Thr Lys	
585 590 595 600	
ctt gaa aaa aag gga gta gga gcg att tta gac ttt ggc gag ctt ggt	1937
Leu Glu Lys Lys Gly Val Gly Ala Ile Leu Asp Phe Gly Glu Leu Gly	
605 610 615	
ttt aag ggt gtt ttg gta gaa aca att gct att gtt aca caa aaa tca	1985
Phe Lys Gly Val Leu Val Glu Thr Ile Ala Ile Val Thr Gln Lys Ser	
620 625 630	
aaa gaa gtt tta gcg cgt tcg tta ccc cta aat cta agc atc aag caa	2033
Lys Glu Val Leu Ala Arg Ser Leu Pro Leu Asn Leu Ser Ile Lys Gln	
635 640 645	
aag cca agc tat att ttt gac aaa caa ttg ccc tat tgg gtt atc tat	2081
Lys Pro Ser Tyr Ile Phe Asp Lys Gln Leu Pro Tyr Trp Val Ile Tyr	
650 655 660	
cgc aac gct ttt ttt gat aag gtg ttt cat tcc atg cag ttt ggt ctt	2129
Arg Asn Ala Phe Phe Asp Lys Val Phe His Ser Met Gln Phe Gly Leu	
665 670 675 680	
ttt gaa gtg ttt aga gac aga caa atc act aat tct gtg ttg gtt aaa	2177
Phe Glu Val Phe Arg Asp Arg Gln Ile Thr Asn Ser Val Leu Val Lys	
685 690 695	
aat ggt att cgt gtg att aaa tct cgc aat att gat gaa aac gga aag	2225
Asn Gly Ile Arg Val Ile Lys Ser Arg Asn Ile Asp Glu Asn Gly Lys	
700 705 710	
att att agc att gaa aat tac gat agc tac att caa aaa gag gtt tta	2273
Ile Ile Ser Ile Glu Asn Tyr Asp Ser Tyr Ile Gln Lys Glu Val Leu	
715 720 725	
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Ser Pro Phe Lys Ile Ala Ser Phe Leu Asp Arg Asp Asp Val Tyr Leu	
730 735 740	
acc ccc aac atg acc tat aag cca agg att tta aaa aaa gaa aaa ggc	2369
Thr Pro Asn Met Thr Tyr Lys Pro Arg Ile Leu Lys Lys Glu Lys Gly	
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Ser Leu Ser Lys Lys Gln Cys Asp Tyr Ile Ser Ser Val Glu Phe Arg	
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gat ttt tat aaa atc gct agg aat tat caa acg cgc acc tta aat att	2513
Asp Phe Tyr Lys Ile Ala Arg Asn Tyr Gln Thr Arg Thr Leu Asn Ile	
795 800 805	
gat agc atg agt tgt ttt tgg ttt gga att tta agg agt agc tta	2558
Asp Ser Met Ser Cys Phe Trp Phe Gly Ile Leu Arg Ser Ser Leu	
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Thr	Asn	Pro	Phe	Ile	Ile	Asn	Glu	Ile	Ala	Lys	Leu	Leu	Pro	Ser	Phe	
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Phe	Leu	Ser	Ala	Leu	Phe	Lys	Lys	Tyr	Thr	Ser	Val	Lys	Lys	Val	Tyr	
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Ala	Asn	Phe	Thr	Ala	Met	Val	Met	Pro	Lys	Asn	Leu	Leu	Asn	Thr	Lys	
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Glu	Tyr	Ala	Glu	Thr	Arg	Thr	Lys	Leu	Glu	Lys	Lys	Gly	Val	Gly	Ala	
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ccg gat tct tat gaa tat ttg aaa aaa ctg cac gct ttt tct aaa gaa Pro Asp Ser Tyr Glu Tyr Leu Lys Lys Leu His Ala Phe Ser Lys Glu 260 265 270			872
agg gtt tta aaa ggg ttg aag ccc att aaa atc cgc ttt gtt aag gga Arg Val Leu Lys Gly Leu Lys Pro Ile Lys Ile Arg Phe Val Lys Gly 275 280 285			920
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tta ccc aca ttt tcc aat aag caa gac acc gat tct aat tac aat aaa Leu Pro Thr Phe Ser Asn Lys Gln Asp Thr Asp Ser Asn Tyr Asn Lys 310 315 320			1016
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ggc gca gcg agt cat aat att ttt gaa atc gct tat gtc tat acg cgt Gly Ala Ala Ser His Asn Ile Phe Glu Ile Ala Tyr Val Tyr Thr Arg 340 345 350			1112
atc cat gcc att aat gat cct gtt gtg tta gag cat ttc agc ttt gaa Ile His Ala Ile Asn Asp Pro Val Val Leu Glu His Phe Ser Phe Glu 355 360 365			1160
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cac aag ctc att ctt tat gcg ccg gtg tgc gat gaa gcg cat ttt aac His Lys Leu Ile Leu Tyr Ala Pro Val Cys Asp Glu Ala His Phe Asn 390 395 400			1256
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gat aat ttc atg aag gct ttc ttt aac ctc aaa gta ggc acg agc gaa Asp Asn Phe Met Lys Ala Phe Phe Asn Leu Lys Val Gly Thr Ser Glu 420 425 430			1352
tgg aaa gat caa gaa caa cgc ttt tta aac agc ctt aaa gga att gcc			1400

**SECRET**

**SECRET**

**00000000000000000000000000000000**



1140	1145	1150	
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Glu Arg Ser Val Ser Ile Ser Tyr His Arg Tyr Gly Asn Leu Gly Ser			
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agg gtt tta agg caa ccc act tgc cac aaa tca tgc tgt gct gaa aaa			3608
Arg Val Leu Arg Gln Pro Thr Cys His Lys Ser Cys Cys Ala Glu Lys			
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 <213> Helicobacter pylori

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Lys Met Gln Lys Leu Leu Asn Asn Pro Glu Asn Lys Val Met Leu Ile	
35 40 45	
Glu Leu Met Asp Arg Ser Phe Arg Cys Leu Asp Asn Lys Ala Arg Phe	
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Glu Met Ile Glu His Val Leu Asp Lys Tyr Lys Ser Arg Glu Ile Phe	
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Asp Thr Lys Ala Met Val Leu Asp Gln Glu Glu Ser Gln Leu Lys Glu	
115 120 125	
Arg Ile Leu Lys Arg Lys Asn Glu Lys Ile Ile Leu Asn Val Asn Phe	
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145 150 155 160	
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180 185 190	
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098591-062901

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Met	His	Lys	Leu	Ile	Leu	Tyr	Ala	Pro	Val	Cys	Asp	Glu	Ala	His	Phe	
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Ser	Asp	Asn	Phe	Met	Lys	Ala	Phe	Phe	Asn	Leu	Lys	Val	Gly	Thr	Ser	
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Ala	Thr	Leu	Asp	Asn	Ala	Thr	His	Arg	Thr	Gln	Asp	Arg	Asn	Ala	Lys	
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Gln	Ser	Gly	His	Thr	Thr	Tyr	Pro	Asn	His	Ser	Phe	Lys	Asn	Glu	Ser	
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Arg	Glu	Lys	Met	Arg	Asn	Ala	Pro	Ile	Leu	Glu	Leu	Tyr	Pro	Glu	Met	
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Ser	Gln	Lys	Ser	Phe	Thr	Glu	Ile	His	Ala	Leu	Met	Ser	Gln	Thr	Ala	
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Glu	Val	Gly	Lys	Thr	Phe	Ala	Glu	Thr	Asp	Ala	Glu	Val	Ser	Glu	Ala	
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Ile	Asp	Phe	Leu	Glu	Phe	Tyr	Pro	Tyr	Ser	Leu	Arg	Val	Leu	Gln	Glu	
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Gln	Asn	Thr	Lys	Thr	Gln	Phe	Thr	Pro	Lys	Gly	Val	Gly	Val	Val	Ile	
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Ala	Pro	Trp	Asn	Phe	Pro	Val	Gly	Ile	Ser	Val	Gly	Thr	Ile	Ala	Ala	
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			660					665					670			
Ser	Val	Thr	Gly	Tyr	Lys	Leu	Cys	Glu	Cys	Phe	Trp	Asp	Ala	Gly	Val	
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Pro	Arg	Asp	Ala	Leu	Ile	Tyr	Leu	Pro	Ser	Lys	Gly	Ser	Asp	Ile	Ser	
	690					695					700					
Glu	His	Leu	Leu	Arg	Asp	Glu	Ser	Ile	Gln	Phe	Ala	Ile	Leu	Thr	Gly	
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Gly	Glu	Asp	Thr	Ala	Tyr	Lys	Met	Leu	Lys	Ala	Asn	Pro	Thr	Leu	Ala	
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Leu	Ser	Ala	Glu	Thr	Gly	Gly	Lys	Asn	Ala	Thr	Ile	Val	Ser	Lys	Met	
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		755					760					765				
Asn	Ser	Gly	Gln	Lys	Cys	Ser	Ala	Thr	Ser	Leu	Leu	Val	Leu	Glu	Lys	
	770					775					780					
Glu	Val	Tyr	Glu	Asp	Glu	Asn	Phe	Lys	Lys	Thr	Leu	Ile	Asp	Ala	Thr	
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05895913 "062901

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Leu Lys Ser Tyr Glu Asn Tyr Glu Ile Pro Val Ser Phe Val Asn Asp
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Asp Phe Thr His Gln Thr Glu Leu Phe Thr Pro Ile Leu Ser Val Met
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Glu Ala Lys Asp Leu Asp Glu Ala Ile Glu Ile Ala Asn Ser Thr Gly
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Tyr Gly Leu Thr Ser Ala Leu Glu Ser Leu Asp Glu Arg Glu Trp Glu
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Tyr Tyr Leu Glu Arg Ile Glu Ala Gly Asn Ile Tyr Ile Asn Lys Pro
      915      920      925
Thr Thr Gly Ala Ile Val Leu Arg Gln Pro Phe Gly Gly Val Lys Lys
      930      935      940
Ser Ala Val Gly Phe Gly Arg Lys Val Gly Ile Phe Asn Tyr Ile Thr
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Gln Phe Val Asn Ile Cys Gln Glu Glu Glu Asp Glu Asn Ala Leu Lys
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Asn Pro Leu Ser Glu Ala Leu Glu Asn Leu Thr Gln Lys Gly Tyr Asp
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Glu His Thr His Glu Leu Lys Arg Ala Ile Phe Met Ala Lys Ser Tyr
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Ala Tyr His Tyr Lys His Glu Phe Ser Gln Thr Lys Asp Tyr Val Lys
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Ile Arg Gly Glu Asp Asn Leu Phe Ser Tyr Thr Lys Val Lys Ser Val
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Gly Tyr Arg Ile Thr Glu Lys Asp Thr Leu Ser Asp Met Leu Gly Val
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Ala Leu Ala Cys Leu Ile Ser Gln Ile Pro Leu Thr Leu Ser Ile Glu
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Asn Glu Arg Thr Asn Lys Asp Leu Thr Phe Phe Leu Glu Cys Leu Lys
      1075      1080      1085
Ala Leu Gln Ala Ser Ala Pro Ile Val Tyr Glu Ser Leu Gln Lys Phe
      1090      1095      1100
Ser Glu Lys Leu Asn Thr Phe Asn Arg Val Arg Tyr Leu Lys Ser Asp
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Leu Asp Leu Leu His Glu Gln Ala Ser Ala Leu Gly Met Val Leu Ala
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Thr Ala Lys Pro Cys Leu Asn Gly Arg Phe Glu Leu Leu Tyr Tyr His
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Leu Glu Arg Ser Val Ser Ile Ser Tyr His Arg Tyr Gly Asn Leu Gly
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aag aac gcg tat gcg ttt gtt gtg att gaa gaa agc gtt atg gtg ttt 163  
Lys Asn Ala Tyr Ala Phe Val Val Ile Glu Glu Ser Val Met Val Phe  
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aaa cgc acc aaa gat gag ggg tta atg cct atc ttt gaa ggc ttt gtg 211  
Lys Arg Thr Lys Asp Glu Gly Leu Met Pro Ile Phe Glu Gly Phe Val  
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cct tta aaa gag ggc ttt ttg aaa agt ttt aaa gag cgt tgc aat ttg 259  
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gaa ttt tta gaa aat tta gac ctt ttg ttt ttg tat gac aaa cca tcc 307  
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55 60 65

gca cac gag atc ttt tcc ttg tgc aag gag ctg aaa aat tcc atc tgg 355  
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Gly Asn Gly Thr Lys Lys Leu Leu Thr Asn Ala Asp Leu Gly Ser Asp  
120 125 130

tat aaa aca atc gtg ata gac agc atg aaa aca tac cac caa agc cag 547  
Tyr Lys Thr Ile Val Ile Asp Ser Met Lys Thr Tyr His Gln Ser Gln  
135 140 145

caa gaa aaa tat aaa aga gaa aga ggc gaa acg cta gag gtt cgc ccc 595  
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165 170 175

aaa aag cct gat ttt gat gaa gaa aat ttt taaaagaaag gacaaccgat 693  
Lys Lys Pro Asp Phe Asp Glu Glu Asn Phe  
180 185

gagcagagtg caaatggata ccgaagaggt caggggaattt gtagggcatt tagaacgctt 753  
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Cys Asn Leu Glu Phe Leu Glu Asn Leu Asp Leu Leu Phe Leu Tyr Asp  
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Gly Ser Asp Tyr Lys Thr Ile Val Ile Asp Ser Met Lys Thr Tyr His  
130 135 140  
Gln Ser Gln Gln Glu Lys Tyr Lys Arg Glu Arg Gly Glu Thr Leu Glu  
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Lys Leu Met Ala Pro Phe Tyr Pro Lys Asp Asp Leu Ala Glu Ile Met  
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Val Gln Leu Asn Ile Gly Pro Asn Cys Lys Leu Arg Ile Thr Ser Gln
 65          70          75          80
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 85          90          95
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100          105          110
Pro Leu Ile Pro Phe Glu Asn Ala His Phe Lys Gly Asn Thr Thr Ile
115          120          125
Ser Leu Arg Ser Ser Ser Gln Leu Leu Tyr Ser Glu Ile Ile Val Ala
130          135          140
Gly Arg Val Ala Arg Asn Glu Leu Phe Lys Phe Asn Arg Leu His Thr
145          150          155          160
Lys Ile Ser Ile Leu Gln Asp Glu Lys Pro Ile Tyr Tyr Asp Asn Thr
165          170          175
Ile Leu Asp Pro Lys Thr Thr Asp Leu Asn Asn Met Cys Met Phe Asp
180          185          190
Gly Tyr Thr His Tyr Leu Asn Leu Val Leu Val Asn Cys Pro Ile Glu
195          200          205
Leu Ser Gly Val Arg Glu Cys Ile Glu Glu Ser Glu Gly Val Asp Gly
210          215          220
Ala Val Ser Glu Thr Ala Ser Ser His Leu Cys Val Lys Ala Leu Ala
225          230          235          240
Lys Gly Ser Glu Pro Leu Leu His Leu Arg Glu Lys Ile Ala Arg Leu
245          250          255
Val Thr Gln Thr Thr Thr Gln Lys Val
260          265

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<210> 251
<211> 1815
<212> DNA
<213> Helicobacter pylori

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<220>
<221> CDS
<222> (51)...(1757)

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<400> 251
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                                         Met Lys
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aag att agc aga aaa gaa tat gtt tct atg tat ggc cct act aca ggc      104
Lys Ile Ser Arg Lys Glu Tyr Val Ser Met Tyr Gly Pro Thr Thr Gly
 5          10          15

gat aaa gtg aga ttg ggc gat aca gac ttg atc gct gaa gta gaa cat      152
Asp Lys Val Arg Leu Gly Asp Thr Asp Leu Ile Ala Glu Val Glu His
 20          25          30

gac tac acc att tat ggc gaa gag ctt aaa ttc ggt ggc ggt aaa acc      200

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Asp 35	Tyr	Thr	Ile	Tyr	Gly 40	Glu	Glu	Leu	Lys	Phe 45	Gly	Gly	Gly	Lys	Thr 50	
ctg Leu	aga Arg	gaa Glu	ggc Gly	atg Met 55	agc Ser	caa Gln	tcc Ser	aac Asn	aac Asn 60	cct Pro	agc Ser	aaa Lys	gaa Glu	gaa Glu 65	ttg Leu	248
gat Asp	cta Leu	atc Ile	atc Ile 70	act Thr	aac Asn	gct Ala	tta Leu	atc Ile 75	gtg Val	gat Asp	tac Tyr	acc Thr	ggg Gly 80	att Ile	tat Tyr	296
aaa Lys	gcg Ala	gat Asp 85	att Ile	ggg Gly	att Ile	aaa Lys	gat Asp 90	ggc Gly	aaa Lys	atc Ile	gct Ala	ggc Gly 95	att Ile	ggg Gly	aaa Lys	344
ggc Gly	ggg Gly 100	aac Asn	aaa Lys	gac Asp	atg Met	caa Gln 105	gat Asp	ggc Gly	gtt Val	aaa Lys	aac Asn 110	aat Asn	ctt Leu	agc Ser	gta Val	392
ggg Gly 115	cct Pro	gct Ala	act Thr	gaa Glu	gcc Ala 120	tta Leu	gcc Ala	ggg Gly	gaa Glu	ggg Gly 125	ttg Leu	atc Ile	gta Val	act Thr	gct Ala 130	440
ggg Gly	ggg Gly	att Ile	gac Asp	aca Thr 135	cac His	atc Ile	cac His	ttc Phe	att Ile 140	tca Ser	ccc Pro	caa Gln	caa Gln	atc Ile 145	cct Pro	488
aca Thr	gct Ala	ttt Phe 150	gca Ala	agc Ser	ggg Gly	gta Val	aca Thr	acc Thr 155	atg Met	att Ile	ggg Gly	ggc Gly 160	gga Gly	act Thr	ggg Gly	536
cct Pro	gct Ala	gat Asp 165	ggc Gly	act Thr	aat Asn	gcg Ala	act Thr 170	act Thr	atc Ile	act Thr	cca Pro	ggc Gly 175	aga Arg	aga Arg	aat Asn	584
tta Leu	aaa Lys 180	tgg Trp	atg Met	ctc Leu	aga Arg	gcg Ala 185	gct Ala	gaa Glu	gaa Glu	tat Tyr	tct Ser 190	atg Met	aac Asn	tta Leu	ggg Gly	632
ttc Phe 195	ttg Leu	gct Ala	aaa Lys	ggg Gly	aac Asn 200	gct Ala	tct Ser	aac Asn	gac Asp	gcg Ala 205	agc Ser	tta Leu	gcc Ala	gat Asp	caa Gln 210	680
att Ile	gaa Glu	gct Ala	ggg Gly	gcg Ala 215	att Ile	ggc Gly	ttt Phe	aaa Lys	atc Ile 220	cac His	gaa Glu	gac Asp	tgg Trp	ggc Gly 225	acc Thr	728
act Thr	cct Pro	tct Ser	gca Ala 230	atc Ile	aat Asn	cat His	gcg Ala	tta Leu 235	gat Asp	gtt Val	gca Ala	gac Asp	aaa Lys 240	tac Tyr	gat Asp	776
gtg Val	caa Gln 245	gtc Val	gct Ala	atc Ile	cac His	aca Thr	gac Asp 250	act Thr	ttg Leu	aat Asn	gaa Glu	gcc Ala 255	ggg Gly	tgc Cys	gtg Val	824
gaa Glu	gac Asp 260	act Thr	atg Met	gca Ala	gct Ala	att Ile 265	gcc Ala	gga Gly	cgc Arg	act Thr	atg Met 270	cac His	act Thr	ttc Phe	cac His	872





ccg gta aaa aat tgc aga aac atc act aaa aaa gac atg caa ttc aac 1640  
 Pro Val Lys Asn Cys Arg Asn Ile Thr Lys Lys Asp Met Gln Phe Asn  
 515 520 525 530

gac act acc gct cac att gaa gtc aat cct gaa act tac cat gtg ttc 1688  
 Asp Thr Thr Ala His Ile Glu Val Asn Pro Glu Thr Tyr His Val Phe  
 535 540 545

gtg gat ggc aaa gaa gta act tct aaa cca gcc aat aaa gtg agc ttg 1736  
 Val Asp Gly Lys Glu Val Thr Ser Lys Pro Ala Asn Lys Val Ser Leu  
 550 555 560

gcg caa ctc ttt agc att ttc taggattttt taggagcaac gctccttaaa 1787  
 Ala Gln Leu Phe Ser Ile Phe  
 565

tccttagttt ttagctctct gatttttt 1815

<210> 252  
 <211> 569  
 <212> PRT  
 <213> Helicobacter pylori

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 20 25 30  
 Glu His Asp Tyr Thr Ile Tyr Gly Glu Glu Leu Lys Phe Gly Gly Gly  
 35 40 45  
 Lys Thr Leu Arg Glu Gly Met Ser Gln Ser Asn Asn Pro Ser Lys Glu  
 50 55 60  
 Glu Leu Asp Leu Ile Ile Thr Asn Ala Leu Ile Val Asp Tyr Thr Gly  
 65 70 75 80  
 Ile Tyr Lys Ala Asp Ile Gly Ile Lys Asp Gly Lys Ile Ala Gly Ile  
 85 90 95  
 Gly Lys Gly Gly Asn Lys Asp Met Gln Asp Gly Val Lys Asn Asn Leu  
 100 105 110  
 Ser Val Gly Gly Pro Ala Thr Glu Ala Leu Ala Gly Glu Gly Leu Ile Val  
 115 120 125  
 Thr Ala Gly Gly Ile Asp Thr His Ile His Phe Ile Ser Pro Gln Gln  
 130 135 140  
 Ile Pro Thr Ala Phe Ala Ser Gly Val Thr Thr Met Ile Gly Gly Gly  
 145 150 155 160  
 Thr Gly Pro Ala Asp Gly Thr Asn Ala Thr Thr Ile Thr Pro Gly Arg  
 165 170 175  
 Arg Asn Leu Lys Trp Met Leu Arg Ala Glu Glu Tyr Ser Met Asn  
 180 185 190  
 Leu Gly Phe Leu Ala Lys Gly Asn Ala Ser Asn Asp Ala Ser Leu Ala  
 195 200 205  
 Asp Gln Ile Glu Ala Gly Ala Ile Gly Phe Lys Ile His Glu Asp Trp  
 210 215 220  
 Gly Thr Thr Pro Ser Ala Ile Asn His Ala Leu Asp Val Ala Asp Lys  
 225 230 235 240  
 Tyr Asp Val Gln Val Ala Ile His Thr Asp Thr Leu Asn Glu Ala Gly  
 245 250 255  
 Cys Val Glu Asp Thr Met Ala Ala Ile Ala Gly Arg Thr Met His Thr  
 260 265 270

05895913-062901

Phe His Thr Glu Gly Ala Gly Gly Gly His Ala Pro Asp Ile Ile Lys  
 275 280 285  
 Val Ala Gly Glu His Asn Ile Leu Pro Ala Ser Thr Asn Pro Thr Ile  
 290 295 300  
 Pro Phe Thr Val Asn Thr Glu Ala Glu His Met Asp Met Leu Met Val  
 305 310 315 320  
 Cys His His Leu Asp Lys Ser Ile Lys Glu Asp Val Gln Phe Ala Asp  
 325 330 335  
 Ser Arg Ile Arg Pro Gln Thr Ile Ala Ala Glu Asp Thr Leu His Asp  
 340 345 350  
 Met Gly Ile Phe Ser Ile Thr Ser Ser Asp Ser Gln Ala Met Gly Arg  
 355 360 365  
 Val Gly Glu Val Ile Thr Arg Thr Trp Gln Thr Ala Asp Lys Asn Lys  
 370 375 380  
 Lys Glu Phe Gly Arg Leu Lys Glu Glu Lys Gly Asp Asn Asp Asn Phe  
 385 390 395 400  
 Arg Ile Lys Arg Tyr Leu Ser Lys Tyr Thr Ile Asn Pro Ala Ile Ala  
 405 410 415  
 His Gly Ile Ser Glu Tyr Val Gly Ser Val Glu Val Gly Lys Val Ala  
 420 425 430  
 Asp Leu Val Leu Trp Ser Pro Ala Phe Phe Gly Val Lys Pro Asn Met  
 435 440 445  
 Ile Ile Lys Gly Gly Phe Ile Ala Leu Ser Gln Met Gly Asp Ala Asn  
 450 455 460  
 Ala Ser Ile Pro Thr Pro Gln Pro Val Tyr Tyr Arg Glu Met Phe Ala  
 465 470 475 480  
 His His Gly Lys Ala Lys Tyr Asp Ala Asn Ile Thr Phe Val Ser Gln  
 485 490 495  
 Ala Ala Tyr Asp Lys Gly Ile Lys Glu Glu Leu Gly Leu Glu Arg Gln  
 500 505 510  
 Val Leu Pro Val Lys Asn Cys Arg Asn Ile Thr Lys Lys Asp Met Gln  
 515 520 525  
 Phe Asn Asp Thr Thr Ala His Ile Glu Val Asn Pro Glu Thr Tyr His  
 530 535 540  
 Val Phe Val Asp Gly Lys Glu Val Thr Ser Lys Pro Ala Asn Lys Val  
 545 550 555 560  
 Ser Leu Ala Gln Leu Phe Ser Ile Phe  
 565

<210> 253  
 <211> 934  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (51)...(881)

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 Ile Ala His Ser Asn Glu Ile Ala Arg Pro Ile Phe Lys Ser Gln Asp  
 5 10 15  
 cag ctt ttc act ctt tat caa ggg gat tgt aat gag gtt ttg ccc caa 152  
 Gln Leu Phe Thr Leu Tyr Gln Gly Asp Cys Asn Glu Val Leu Pro Gln

20				25				30								
ttt	gaa	aac	cag	ttt	gat	ttg	att	ttt	gct	gat	ccg	cct	tat	ttc	ctc	200
Phe	Glu	Asn	Gln	Phe	Asp	Leu	Ile	Phe	Ala	Asp	Pro	Pro	Tyr	Phe	Leu	
35					40					45					50	
tct	aat	gac	ggc	tta	agc	ata	cag	agc	ggg	aaa	atc	gtg	agc	gtc	aat	248
Ser	Asn	Asp	Gly	Leu	Ser	Ile	Gln	Ser	Gly	Lys	Ile	Val	Ser	Val	Asn	
				55					60					65		
aaa	ggc	gat	tgg	gat	aaa	gaa	gat	ggg	att	aat	ggg	att	gat	gag	ttt	296
Lys	Gly	Asp	Trp	Asp	Lys	Glu	Asp	Gly	Ile	Asn	Gly	Ile	Asp	Glu	Phe	
			70					75					80			
aat	tac	cag	tgg	ata	aac	aac	gct	aaa	aag	gct	tta	aaa	gac	aca	gga	344
Asn	Tyr	Gln	Trp	Ile	Asn	Asn	Ala	Lys	Lys	Ala	Leu	Lys	Asp	Thr	Gly	
		85					90					95				
agc	ctt	tta	atc	agc	ggg	act	tac	cac	aac	atc	ttt	tct	ttg	ggg	tgt	392
Ser	Leu	Leu	Ile	Ser	Gly	Thr	Tyr	His	Asn	Ile	Phe	Ser	Leu	Gly	Cys	
	100					105					110					
gtt	tta	caa	aaa	ttg	gat	ttt	aag	att	tta	aac	ctc	atc	acc	tgg	caa	440
Val	Leu	Gln	Lys	Leu	Asp	Phe	Lys	Ile	Leu	Asn	Leu	Ile	Thr	Trp	Gln	
115					120					125					130	
aaa	acc	aac	cct	cct	ccc	aat	ttc	agc	tgc	cgt	tat	ttg	acg	cat	tca	488
Lys	Thr	Asn	Pro	Pro	Pro	Asn	Phe	Ser	Cys	Arg	Tyr	Leu	Thr	His	Ser	
			135						140					145		
gct	gag	caa	atc	att	tgg	gcg	aga	aaa	agc	cgc	aaa	cac	aag	cat	gtt	536
Ala	Glu	Gln	Ile	Ile	Trp	Ala	Arg	Lys	Ser	Arg	Lys	His	Lys	His	Val	
			150					155					160			
ttt	aac	tat	gag	gtt	tta	aaa	aag	atc	aat	aac	gac	aag	caa	atg	cgc	584
Phe	Asn	Tyr	Glu	Val	Leu	Lys	Lys	Ile	Asn	Asn	Asp	Lys	Gln	Met	Arg	
		165					170					175				
gat	gtg	tgg	agc	ttc	cca	gcg	atc	gct	cct	tgg	gaa	aaa	gtt	aat	ggc	632
Asp	Val	Trp	Ser	Phe	Pro	Ala	Ile	Ala	Pro	Trp	Glu	Lys	Val	Asn	Gly	
	180					185					190					
aag	cac	ccc	act	caa	aaa	ccc	ctc	gct	tta	tta	gtg	cgc	ttg	ctt	tta	680
Lys	His	Pro	Thr	Gln	Lys	Pro	Leu	Ala	Leu	Leu	Val	Arg	Leu	Leu	Leu	
195					200					205					210	
atg	gcg	agc	gat	gaa	aat	tct	ctc	att	ggc	gat	cct	ttt	agc	ggg	agc	728
Met	Ala	Ser	Asp	Glu	Asn	Ser	Leu	Ile	Gly	Asp	Pro	Phe	Ser	Gly	Ser	
				215					220					225		
tct	acc	aca	ggc	att	gcg	gct	aat	ctt	ttg	aag	agg	gaa	ttt	att	ggc	776
Ser	Thr	Thr	Gly	Ile	Ala	Ala	Asn	Leu	Leu	Lys	Arg	Glu	Phe	Ile	Gly	
			230					235					240			
ata	gaa	aaa	gaa	agc	gag											

Glu Leu Asp Ala Arg Tyr Lys Glu Ile Arg Ser Lys Ile Lys Asp Leu  
 260 265 270

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 Asn His Gln  
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921

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934

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 <211> 277  
 <212> PRT  
 <213> Helicobacter pylori

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 20 25 30  
 Pro Gln Phe Glu Asn Gln Phe Asp Leu Ile Phe Ala Asp Pro Pro Tyr  
 35 40 45  
 Phe Leu Ser Asn Asp Gly Leu Ser Ile Gln Ser Gly Lys Ile Val Ser  
 50 55 60  
 Val Asn Lys Gly Asp Trp Asp Lys Glu Asp Gly Ile Asn Gly Ile Asp  
 65 70 75 80  
 Glu Phe Asn Tyr Gln Trp Ile Asn Asn Ala Lys Lys Ala Leu Lys Asp  
 85 90 95  
 Thr Gly Ser Leu Leu Ile Ser Gly Thr Tyr His Asn Ile Phe Ser Leu  
 100 105 110  
 Gly Cys Val Leu Gln Lys Leu Asp Phe Lys Ile Leu Asn Leu Ile Thr  
 115 120 125  
 Trp Gln Lys Thr Asn Pro Pro Asn Phe Ser Cys Arg Tyr Leu Thr  
 130 135 140  
 His Ser Ala Glu Gln Ile Ile Trp Ala Arg Lys Ser Arg Lys His Lys  
 145 150 155 160  
 His Val Phe Asn Tyr Glu Val Leu Lys Lys Ile Asn Asn Asp Lys Gln  
 165 170 175  
 Met Arg Asp Val Trp Ser Phe Pro Ala Ile Ala Pro Trp Glu Lys Val  
 180 185 190  
 Asn Gly Lys His Pro Thr Gln Lys Pro Leu Ala Leu Leu Val Arg Leu  
 195 200 205  
 Leu Leu Met Ala Ser Asp Glu Asn Ser Leu Ile Gly Asp Pro Phe Ser  
 210 215 220  
 Gly Ser Ser Thr Thr Gly Ile Ala Ala Asn Leu Leu Lys Arg Glu Phe  
 225 230 235 240  
 Ile Gly Ile Glu Lys Glu Ser Glu Phe Ile Lys Ile Ser Met Asp Arg  
 245 250 255  
 Lys Ile Glu Leu Asp Ala Arg Tyr Lys Glu Ile Arg Ser Lys Ile Lys  
 260 265 270  
 Asp Leu Asn His Gln  
 275

<210> 255  
 <211> 646  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS

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aaagaggaa	aatatcagtg	caagctttct	ttgattttag	ccgctaaaaa	cagcgtgttt	180
gtgcataata	gaagagggga	ttaatgtggg	attggctgtc	agcttgggat	tgacatcaaa	240
aaaaaggcgc	ttgagtat	atg gca aag	cgc gtg cca	aac atg gag	ctt ttt	291

gtg ttt tgc gaa gac tta gaa ttc acg caa aat ctt gat ctt ggc tac 339  
Val Phe Cys Glu Asp Leu Glu Phe Thr Gln Asn Leu Asp Leu Gly Tyr  
15 20 25

cct ttt atg gac atg acc act agg gat aaa gaa gaa gag gcg tat tgg 387  
Pro Phe Met Asp Met Thr Thr Arg Asp Lys Glu Glu Glu Ala Tyr Trp  
30 35 40

gac atg ctg ctc atg caa tct tgt cag cat ggc att atc gct aat agc 435  
Asp Met Leu Leu Met Gln Ser Cys Gln His Gly Ile Ile Ala Asn Ser  
45 50 55

act tat agc tgg tgg gcg gcc tat ttg ata gaa aat cca gaa aaa atc 483  
Thr Tyr Ser Trp Trp Ala Ala Tyr Leu Ile Glu Asn Pro Glu Lys Ile  
60 65 70 75

att att ggc ccc aaa cac tgg ctt ttt ggg cat gag aat atc ctt tgt 531  
Ile Ile Gly Pro Lys His Trp Leu Phe Gly His Glu Asn Ile Leu Cys  
80 85 90

aag gag tgg gtg aaa ata gaa tcc cat ttt gag gta aaa tcc caa aag 579  
Lys Glu Trp Val Lys Ile Glu Ser His Phe Glu Val Lys Ser Gln Lys  
95 100 105

tat aac gct taaagtggct taaaaaagg ctttattggt ggtttaaatc 628  
Tyr Asn Ala  
110

tttgatttta gatcggat 646

 $\langle 211 \rangle$  110

<213> Helicobacter pylori

Met	Ala	Lys	Arg	Val	Pro	Asn	Met	Glu	Leu	Phe	Val	Phe	Cys	Glu	Asp
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Leu	Glu	Phe	Thr	Gln	Asn	Leu	Asp	Leu	Gly	Tyr	Pro	Phe	Met	Asp	Met
			20					25					30		
Thr	Thr	Arg	Asp	Lys	Glu	Glu	Glu	Ala	Tyr	Trp	Asp	Met	Leu	Leu	Met
			35				40					45			
Gln	Ser	Cys	Gln	His	Gly	Ile	Ile	Ala	Asn	Ser	Thr	Tyr	Ser	Trp	Trp
	50					55					60				
Ala	Ala	Tyr	Leu	Ile	Glu	Asn	Pro	Glu	Lys	Ile	Ile	Ile	Gly	Pro	Lys
65					70					75				80	
His	Trp	Leu	Phe	Gly	His	Glu	Asn	Ile	Leu	Cys	Lys	Glu	Trp	Val	Lys
				85					90					95	

Ile Glu Ser His Phe Glu Val Lys Ser Gln Lys Tyr Asn Ala  
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<210> 257  
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 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (51)...(974)

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 1  
 aaa gaa aat ccg cct atc gtt ttt ggg cct gtt tta tcc agg cgt ttt 104  
 Lys Glu Asn Pro Pro Ile Val Phe Gly Pro Val Leu Ser Arg Arg Phe  
 5 10 15  
 ggg aag tct ttg ggc gtg gat cta tcg ccc tct aaa aaa caa tgc aat 152  
 Gly Lys Ser Leu Gly Val Asp Leu Ser Pro Ser Lys Lys Gln Cys Asn  
 20 25 30  
 tac aat tgc att tat tgc gag ttg ggt aaa gcc aag ccc att gaa cgc 200  
 Tyr Asn Cys Ile Tyr Cys Glu Leu Gly Lys Ala Lys Pro Ile Glu Arg  
 35 40 45 50  
 atg gaa gaa gtg atc aaa gtg gaa acc ttg att aac gcc att caa aac 248  
 Met Glu Glu Val Ile Lys Val Glu Thr Leu Ile Asn Ala Ile Gln Asn  
 55 60 65  
 gcc cta aac aac ctc acc acc ccc att gat gtt tta acc att acc gct 296  
 Ala Leu Asn Asn Leu Thr Thr Pro Ile Asp Val Leu Thr Ile Thr Ala  
 70 75 80  
 aat ggc gaa ccc acg cta tac cct cat tta tta gag ctt atc caa agc 344  
 Asn Gly Glu Pro Thr Leu Tyr Pro His Leu Leu Glu Leu Ile Gln Ser  
 85 90 95  
 atc aag cct ttt tta aag ggc gtt aaa act ttg att tta agc aat ggc 392  
 Ile Lys Pro Phe Leu Lys Gly Val Lys Thr Leu Ile Leu Ser Asn Gly  
 100 105 110  
 tcg ctc ttt tat gag cca aaa gtc cag caa gcc tta aag gaa ttt gac 440  
 Ser Leu Phe Tyr Glu Pro Lys Val Gln Gln Ala Leu Lys Glu Phe Asp  
 115 120 125 130  
 atc gtt aaa ttt tct tta gac gct att gat ttg aaa gcc ttt gaa aga 488  
 Ile Val Lys Phe Ser Leu Asp Ala Ile Asp Leu Lys Ala Phe Glu Arg  
 135 140 145  
 gtg gat aaa ccc tat tct aaa gac att aat aag att tta gag ggc att 536  
 Val Asp Lys Pro Tyr Ser Lys Asp Ile Asn Lys Ile Leu Glu Gly Ile  
 150 155 160  
 ttg cgc ttt tct caa att tat caa ggg caa ttg gtg gct gaa gtg ttg 584  
 Leu Arg Phe Ser Gln Ile Tyr Gln Gly Gln Leu Val Ala Glu Val Leu

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165	170	175	
tta att aag ggc gtg aat gat agc gcg aac aac tta aaa ctc atc gct Leu Ile Lys Gly Val Asn Asp Ser Ala Asn Asn Leu Lys Leu Ile Ala 180 185 190			632
gcc ttt tta aaa caa atc aat ata gcc aga gtg gat tta agc acc ata Ala Phe Leu Lys Gln Ile Asn Ile Ala Arg Val Asp Leu Ser Thr Ile 195 200 205 210			680
gac aga ccc tca agc ttt aaa gcc cct aaa tta agc gaa gat gaa ttg Asp Arg Pro Ser Ser Phe Lys Ala Pro Lys Leu Ser Glu Asp Glu Leu 215 220 225			728
tta aaa tgc tct tta ttt ttt gaa ggg ctt tgc gtg agt ttg cct aaa Leu Lys Cys Ser Leu Phe Phe Glu Gly Leu Cys Val Ser Leu Pro Lys 230 235 240			776
cga tcc att act caa gct aaa aaa ttg att tct tgc ggt ata gac gaa Arg Ser Ile Thr Gln Ala Lys Lys Leu Ile Ser Cys Gly Ile Asp Glu 245 250 255			824
ttg ctc gct tta att tcc agg cgc cct tta agc gca gaa gaa gcc ccc Leu Leu Ala Leu Ile Ser Arg Arg Pro Leu Ser Ala Glu Glu Ala Pro 260 265 270			872
cta att cta gat tct aac gct ttt aag cat tta gaa act ttg tta aac Leu Ile Leu Asp Ser Asn Ala Phe Lys His Leu Glu Thr Leu Leu Asn 275 280 285 290			920
cat aag caa att acg att aaa aaa gtc ggc tct ttg gag ttt tat tgc His Lys Gln Ile Thr Ile Lys Lys Val Gly Ser Leu Glu Phe Tyr Cys 295 300 305			968
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aaa			1027
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Arg Phe Gly Lys Ser Leu Gly Val Asp Leu Ser Pro Ser Lys Lys Gln 20 25 30			
Cys Asn Tyr Asn Cys Ile Tyr Cys Glu Leu Gly Lys Ala Lys Pro Ile 35 40 45			
Glu Arg Met Glu Glu Val Ile Lys Val Glu Thr Leu Ile Asn Ala Ile 50 55 60			
Gln Asn Ala Leu Asn Asn Leu Thr Thr Pro Ile Asp Val Leu Thr Ile 65 70 75 80			
Thr Ala Asn Gly Glu Pro Thr Leu Tyr Pro His Leu Leu Glu Leu Ile 85 90 95			
Gln Ser Ile Lys Pro Phe Leu Lys Gly Val Lys Thr Leu Ile Leu Ser			



Asn Gly Ser Leu Phe Tyr Glu Pro Lys Val Gln Gln Ala Leu Lys Glu	100	105	110
Phe Asp Ile Val Lys Phe Ser Leu Asp Ala Ile Asp Leu Lys Ala Phe	115	120	125
Glu Arg Val Asp Lys Pro Tyr Ser Lys Asp Ile Asn Lys Ile Leu Glu	130	135	140
Gly Ile Leu Arg Phe Ser Gln Ile Tyr Gln Gly Gln Leu Val Ala Glu	145	150	155
Val Leu Leu Ile Lys Gly Val Asn Asp Ser Ala Asn Asn Leu Lys Leu	165	170	175
Ile Ala Ala Phe Leu Lys Gln Ile Asn Ile Ala Arg Val Asp Leu Ser	180	185	190
Thr Ile Asp Arg Pro Ser Ser Phe Lys Ala Pro Lys Leu Ser Glu Asp	195	200	205
Glu Leu Leu Lys Cys Ser Leu Phe Phe Glu Gly Leu Cys Val Ser Leu	210	215	220
Pro Lys Arg Ser Ile Thr Gln Ala Lys Lys Leu Ile Ser Cys Gly Ile	225	230	235
Asp Glu Leu Leu Ala Leu Ile Ser Arg Arg Pro Leu Ser Ala Glu Glu	245	250	255
Ala Pro Leu Ile Leu Asp Ser Asn Ala Phe Lys His Leu Glu Thr Leu	260	265	270
Leu Asn His Lys Gln Ile Thr Ile Lys Lys Val Gly Ser Leu Glu Phe	275	280	285
Tyr Cys Ala Phe	290	295	300
305			

<210> 259  
 <211> 1350  
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 <213> Helicobacter pylori

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aat aag gtt ggc aag aat aca gag atg gct aat aca aag gca aat aaa	161
Asn Lys Val Gly Lys Asn Thr Glu Met Ala Asn Thr Lys Ala Asn Lys	
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Glu Thr His Phe Lys Gln Val Ser Ala Ile Thr Asn Ile Ile Arg Ser	
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gtt ggt ggg ttt ttt aca aaa att gca aag aga gtt aga gga ctt gta	257
Val Gly Gly Phe Phe Thr Lys Ile Ala Lys Arg Val Arg Gly Leu Val	
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Lys Lys His Pro Lys Lys Ser Ser Ala Ala Leu Val Val Leu Thr His	
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Ser Lys Gln Ala Glu Lys Glu Asn Gln Ile Asn Trp Trp Lys Tyr Ser	
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Gly Leu Thr Ile Ala Ala Ser Leu Leu Leu Ala Ala Cys Ser Ala Gly	
110 115 120	
gat act gat aaa cag ata gaa cta gaa caa gaa aaa aag gaa gct gaa	497
Asp Thr Asp Lys Gln Ile Glu Leu Glu Gln Glu Lys Lys Glu Ala Glu	
125 130 135	
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Lys Ala Glu Gln Glu Arg Gln Lys Thr Glu Gln Glu Lys Gln Lys Ala	
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Gly Ile Lys Gly Gly Ile Ala Ile Glu Val Glu Ala Glu Cys Lys Thr	
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 Arg His Ser Cys Ala His Leu Leu Ala Gln Ser Leu Lys Ala Leu Tyr  
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Tyr	Asp	Phe	Lys	Thr	Ser	Ser	Lys	Ile	Ser	Glu	Glu	Asp	Leu	Pro	Lys	
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Phe Thr Gln Asp Asp Ala His Ile Phe Cys Ser Phe Glu Gln Ile Gln	
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Ala Leu Lys Glu His Arg Ile Asp Tyr Lys Ile Asp Glu Gly Gly Gly	
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535 540 545	
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56



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Pro Ile Val Lys Val Gly Arg Ile Ala Gly Gln Phe Ala Lys Pro Arg	
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Glu Arg Met Leu Lys Ala Tyr His Gln Ser Val Ala Thr Leu Asn Leu	
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Cys Gly Val Glu Ile Glu Arg Thr Pro Ile Leu Arg Glu Val Glu Phe	
135 140 145	
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260	265	270	
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Thr Ser Leu Gly Val Lys Thr Arg Ala Phe Asp Ser Val Leu Asp Glu			
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115 120 125			
Arg Ala Cys Gly Val Glu Ile Glu Arg Thr Pro Ile Leu Arg Glu Val			

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His Met Leu Trp Ile Gly	Glu Arg Thr Arg Asp	Pro Lys Gly Ala His
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260	265	270
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275	280	285
Asp Glu Val Lys Ser Phe	Phe Glu Ile His Arg	Ala Glu Gly Ser Leu
290	295	300
Ala Ser Gly Val His Leu	Glu Met Thr Gly Glu	Asn Val Thr Glu Cys
305	310	315
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325	330	335
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Ala Val Arg Leu Gly Pro Pro Ile Arg Ser Met Phe Val Gly Asn Ala	
5 10 15	
ccg ttt tgg ctt tgg ttt ttt aaa gct tgc atg cct tca ctc aaa ttg	152
Pro Phe Trp Leu Trp Phe Phe Lys Ala Cys Met Pro Ser Leu Lys Leu	
20 25 30	
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Arg Thr Met Asp Ser Phe Phe Asn Lys Met Met Gln Leu Arg Val Met	
35 40 45 50	
agc gaa agc aat cgc ggg ctt gca tgc gaa gag acc gcc cca atc atg	248
Ser Glu Ser Asn Arg Gly Leu Ala Cys Glu Glu Thr Ala Pro Ile Met	
55 60 65	



tca	agc	ttc	ctt	tac	ggc	ttt	ctt	tat	ggc	tta	tgg	ccg	atc	gct	tgg	296
Ser	Ser	Phe	Leu	Tyr	Gly	Phe	Leu	Tyr	Gly	Leu	Trp	Pro	Ile	Ala	Trp	
			70					75					80			
atc	att	att	gcg	gcg	att	ttt	tta	tac	aaa	ctc	agc	gtt	aaa	tcc	ggc	344
Ile	Ile	Ile	Ala	Ala	Ile	Phe	Leu	Tyr	Lys	Leu	Ser	Val	Lys	Ser	Gly	
		85					90					95				
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Tyr	Phe	Glu	Ile	Leu	Lys	Glu	Ser	Val	Gln	Ser	Ile	Thr	Leu	Asp	His	
	100					105					110					
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Arg	Ile	Leu	Val	Ile	Leu	Ile	Gly	Phe	Cys	Phe	Gly	Ser	Phe	Leu	Glu	
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Gly	Ala	Ile	Gly	Phe	Gly	Gly	Pro	Ile	Ala	Ile	Thr	Ala	Ala	Ile	Leu	
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Val	Gly	Leu	Gly	Leu	Ser	Pro	Leu	Tyr	Ser	Ala	Gly	Leu	Cys	Leu	Ile	
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Ala	Asn	Thr	Ala	Pro	Val	Ala	Phe	Gly	Ala	Val	Gly	Ile	Pro	Ile	Ser	
		165					170					175				
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Ala	Met	Ala	Ser	Ala	Val	Gly	Val	Pro	Ala	Ile	Leu	Ile	Ser	Ala	Met	
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Thr	Gly	Lys	Ile	Leu	Phe	Phe	Val	Ser	Leu	Leu	Val	Pro	Phe	Phe	Ile	
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Val	Phe	Leu	Met	Asp	Gly	Phe	Lys	Gly	Ile	Lys	Glu	Thr	Phe	Pro	Ala	
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Val	Phe	Ile	Ala	Ala	Phe	Ser	Phe	Ala	Gly	Ala	Gln	Phe	Leu	Ser	Ser	
			230					235					240			
aat	tat	tta	ggg	cca	gaa	ttg	cct	ggt	att	att	tca	gcc	ctt	gtt	tca	824
Asn	Tyr	Leu	Gly	Pro	Glu	Leu	Pro	Gly	Ile	Ile	Ser	Ala	Leu	Val	Ser	
		245					250					255				
ctc	gtt	gca	aca	gcg	ctc	ttt	ttg	aaa	ttt	tgg	cag	cct	aaa	gcg	att	872
Leu	Val	Ala	Thr	Ala	Leu	Phe	Leu	Lys	Phe	Trp	Gln	Pro	Lys	Ala	Ile	
		260				265					270					
ttt	aga	agc	gac	ggc	aaa	gcg	gct	tcg	ttc	act	a					

295										300										305										
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Val	Ile	Val	Leu	Trp	Ile	Gln	Pro	Phe	Phe	Lys	Ala	Leu	Phe	Glu	Lys															
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Asp	Gly	Leu	Leu	Ala	Phe	Ser	Asn	Phe	Tyr	Phe	Glu	Phe	Asn	Asn	Ile															
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agt	aac	cac	atc	ttt	aaa	agc	ccg	cct	ttt	gta	gaa	gcc	aat	caa	agc		1112													
Ser	Asn	His	Ile	Phe	Lys	Ser	Pro	Pro	Phe	Val	Glu	Ala	Asn	Gln	Ser															
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cgt	tac	ccc	att	ctc	acc	att	ggc	tta	gtc	tta	agc	ttt	gcc	tat	gtg		1304													
Arg	Tyr	Pro	Ile	Leu	Thr	Ile	Gly	Leu	Val	Leu	Ser	Phe	Ala	Tyr	Val															
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tct	aat	tac	agc	ggg	att	tct	tcc	act	cta	gcc	tta	gcg	ctc	acg	cat		1352													
Ser	Asn	Tyr	Ser	Gly	Ile	Ser	Ser	Thr	Leu	Ala	Leu	Ala	Leu	Thr	His															
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Thr	Gly	Leu	Ala	Phe	Thr	Phe	Phe	Ser	Pro	Leu	Ile	Gly	Trp	Val	Gly															
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Val	Phe	Leu	Thr	Gly	Ser	Asp	Thr	Ser	Ser	Asn	Leu	Leu	Phe	Gly	Ser															
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tta	cag	caa	ctc	acc	gcc	caa	cga	ttg	cac	ctc	cct	gag	gtt	tta	acc		1496													
Leu	Gln	Gln	Leu	Thr	Ala	Gln	Arg	Leu	His	Leu	Pro	Glu	Val	Leu	Thr															
			470					475					480																	
cta	acg	gct	aat	acc	gtg	ggc	ggc	act	tta	ggc	aag	atg	ata	agc	cct		1544													
Leu	Thr	Ala	Asn	Thr	Val	Gly	Gly	Thr	Leu	Gly	Lys	Met	Ile	Ser	Pro															
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caa	agc	atc	gct	atc	gct	tgc	gcg	gcg	gtg	ggg	tta	gcc	ggg	aaa	gag		1592													
Gln	Ser	Ile	Ala	Ile	Ala	Cys	Ala	Ala	Val	Gly	Leu	Ala	Gly	Lys	Glu															
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agc	gat	ttg	ttc	aaa	ttc	acg	gtt	aaa	tac	tcc	ctt	att	ttt	gta	gcg		1640													
Ser	Asp	Leu	Phe	Lys	Phe	Thr	Val	Lys	Tyr	Ser	Leu	Ile	Phe	Val	Ala															
515					520				525						530															
atc	atg	gga	gtt	gtg	atc	agc	gcg	att	gcg	tat	ttg	atc	cct	gaa	gtg		1688													

Ile Met Gly Val Val Ile Ser Ala Ile Ala Tyr Leu Ile Pro Glu Val  
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Val Pro Ala Ile Lys  
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<213> Helicobacter pylori

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20 25 30  
Met Val Phe Lys Leu Lys Gly Tyr Thr Ala Ala Phe Leu Ser Val Ala  
35 40 45  
Leu Ser Ala Val Ile Ala Val Leu Val Tyr Lys Met Pro Val Ser Met  
50 55 60  
Val Gly Ser Ser Phe Leu Tyr Gly Phe Leu Tyr Gly Leu Trp Pro Ile  
65 70 75 80  
Ala Trp Ile Ile Ile Ala Ala Ile Phe Leu Tyr Lys Leu Ser Val Lys  
85 90 95  
Ser Gly Tyr Phe Glu Ile Leu Lys Glu Ser Val Gln Ser Ile Thr Leu  
100 105 110  
Asp His Arg Ile Leu Val Ile Leu Ile Gly Phe Cys Phe Gly Ser Phe  
115 120 125  
Leu Glu Gly Ala Ile Gly Phe Gly Gly Pro Ile Ala Ile Thr Ala Ala  
130 135 140  
Ile Leu Val Gly Leu Gly Leu Ser Pro Leu Tyr Ser Ala Gly Leu Cys  
145 150 155 160  
Leu Ile Ala Asn Thr Ala Pro Val Ala Phe Gly Ala Val Gly Ile Pro  
165 170 175  
Ile Ser Ala Met Ala Ser Ala Val Gly Val Pro Ala Ile Leu Ile Ser  
180 185 190  
Ala Met Thr Gly Lys Ile Leu Phe Val Ser Leu Leu Val Pro Phe  
195 200 205  
Phe Ile Val Phe Leu Met Asp Gly Phe Lys Gly Ile Lys Glu Thr Phe  
210 215 220  
Pro Ala Val Phe Ile Ala Ala Phe Ser Phe Ala Gly Ala Gln Phe Leu  
225 230 235 240  
Ser Ser Asn Tyr Leu Gly Pro Glu Leu Pro Gly Ile Ile Ser Ala Leu  
245 250 255  
Val Ser Leu Val Ala Thr Ala Leu Phe Leu Lys Phe Trp Gln Pro Lys  
260 265 270  
Ala Ile Phe Arg Ser Asp Gly Lys Ala Ala Ser Phe Thr Lys Ser Asn  
275 280 285  
His His Ile Cys Lys Ile Tyr Val Ala Trp Ser Pro Phe Val Ile Leu  
290 295 300  
Val Leu Val Ile Val Leu Trp Ile Gln Pro Phe Phe Lys Ala Leu Phe  
305 310 315 320  
Glu Lys Asp Gly Leu Leu Ala Phe Ser Asn Phe Tyr Phe Glu Phe Asn  
325 330 335  
Asn Ile Ser Asn His Ile Phe Lys Ser Pro Pro Phe Val Glu Ala Asn  
340 345 350

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Gln Ser Val Ser Phe Pro Val Val Phe Lys Phe Leu Leu Ile Asn Thr  
 355 360 365  
 Val Gly Thr Ser Ile Phe Leu Ala Ala Leu Val Ser Met Leu Val Leu  
 370 375 380  
 Arg Val Arg Val Ser Asp Ala Leu Ser Val Phe Gly Glu Thr Leu Lys  
 385 390 395 400  
 Glu Met Arg Tyr Pro Ile Leu Thr Ile Gly Leu Val Leu Ser Phe Ala  
 405 410 415  
 Tyr Val Ser Asn Tyr Ser Gly Ile Ser Ser Thr Leu Ala Leu Ala Leu  
 420 425 430  
 Thr His Thr Gly Leu Ala Phe Thr Phe Phe Ser Pro Leu Ile Gly Trp  
 435 440 445  
 Val Gly Val Phe Leu Thr Gly Ser Asp Thr Ser Ser Asn Leu Leu Phe  
 450 455 460  
 Gly Ser Leu Gln Gln Leu Thr Ala Gln Arg Leu His Leu Pro Glu Val  
 465 470 475 480  
 Leu Thr Leu Thr Ala Asn Thr Val Gly Gly Thr Leu Gly Lys Met Ile  
 485 490 495  
 Ser Pro Gln Ser Ile Ala Ile Ala Cys Ala Ala Val Gly Leu Ala Gly  
 500 505 510  
 Lys Glu Ser Asp Leu Phe Lys Phe Thr Val Lys Tyr Ser Leu Ile Phe  
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 Phe Leu Asn Asp His Ile Asn Val Phe Gly Leu Ile Ala Ala Leu Val  
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 att tta gtt tta acc atc tat gaa tcc agt tcg ctc att aaa gaa atg 152  
 Ile Leu Val Leu Thr Ile Tyr Glu Ser Ser Ser Leu Ile Lys Glu Met  
 20 25 30  
 cgc gac agc aaa tct caa ggt gag ctt gta gaa aat ggg cat ttg att 200  
 Arg Asp Ser Lys Ser Gln Gly Glu Leu Val Glu Asn Gly His Leu Ile  
 35 40 45 50  
 gat ggg ata ggg gag ttt gcc aat aat gtg cca gta ggc tgg atc gca 248  
 Asp Gly Ile Gly Glu Phe Ala Asn Asn Val Pro Val Gly Trp Ile Ala  
 55 60 65  
 agc ttt atg tgc acg att gtg tgg gct ttt tgg tat ttc ttc ttt ggg 296  
 Ser Phe Met Cys Thr Ile Val Trp Ala Phe Trp Tyr Phe Phe Phe Gly



70					75					80						
tat	ccg	ctg	aat	agc	ttt	tct	caa	atc	ggg	caa	tac	aat	gaa	gag	gtt	344
Tyr	Pro	Leu	Asn	Ser	Phe	Ser	Gln	Ile	Gly	Gln	Tyr	Asn	Glu	Glu	Val	
		85					90					95				
aaa	gcg	cac	aac	caa	aaa	ttt	gag	gcc	aag	tgg	aag	cat	ttg	ggt	caa	392
Lys	Ala	His	Asn	Gln	Lys	Phe	Glu	Ala	Lys	Trp	Lys	His	Leu	Gly	Gln	
	100					105					110					
aag	gaa	ctg	gtg	gat	atg	ggg	caa	ggc	atc	ttt	tta	gtc	cat	tgt	tcg	440
Lys	Glu	Leu	Val	Asp	Met	Gly	Gln	Gly	Ile	Phe	Leu	Val	His	Cys	Ser	
					120					125					130	
caa	tgc	cat	ggc	atc	acc	gct	gag	ggc	ttg	cat	ggg	agc	gct	caa	aat	488
Gln	Cys	His	Gly	Ile	Thr	Ala	Glu	Gly	Leu	His	Gly	Ser	Ala	Gln	Asn	
				135					140					145		
ctg	gtg	cgc	tgg	ggg	aaa	gaa	gag	ggg	att	atg	gat	acc	att	aag	cat	536
Leu	Val	Arg	Trp	Gly	Lys	Glu	Glu	Gly	Ile	Met	Asp	Thr	Ile	Lys	His	
			150					155					160			
ggc	tct	aag	ggc	atg	gat	tat	ctc	gct	ggg	gaa	atg	ccc	gct	atg	gaa	584
Gly	Ser	Lys	Gly	Met	Asp	Tyr	Leu	Ala	Gly	Glu	Met	Pro	Ala	Met	Glu	
		165					170					175				
ttg	gac	gaa	aaa	gac	gct	aaa	gcg	atc	gca	agc	tat	gtg	atg	gca	gaa	632
Leu	Asp	Glu	Lys	Asp	Ala	Lys	Ala	Ile	Ala	Ser	Tyr	Val	Met	Ala	Glu	
	180					185					190					
ctt	tct	agc	gtt	aaa	aaa	acc	aaa	aac	cct	caa	ctc	att	gat	aaa	ggc	680
Leu	Ser	Ser	Val	Lys	Lys	Thr	Lys	Asn	Pro	Gln	Leu	Ile	Asp	Lys	Gly	
	195				200					205					210	
aag	gaa	ttg	ttt	gaa	agc	atg	ggg	tgc	aca	ggc	tgt	cat	ggc	aat	gat	728
Lys	Glu	Leu	Phe	Glu	Ser	Met	Gly	Cys	Thr	Gly	Cys	His	Gly	Asn	Asp	
				215					220					225		
ggg	aag	ggc	ttg	caa	gaa	aat	caa	gtg	ttt	gca	gcc	gat	ttg	acc	gct	776
Gly	Lys	Gly	Leu	Gln	Glu	Asn	Gln	Val	Phe	Ala	Ala	Asp	Leu	Thr	Ala	
			230					235					240			
tac	ggc	aca	gag	aat	ttt	ttg	aga	aat	atc	tta	acg	cat	ggc	aaa	aag	824
Tyr	Gly	Thr	Glu	Asn	Phe	Leu	Arg	Asn	Ile	Leu	Thr	His	Gly	Lys	Lys	
		245					250					255				
ggc	aat	ata	ggg	cat	atg	cca	tca	ttc	aag	tat	aaa	aac	ttt	agc	gat	872
Gly	Asn	Ile	Gly	His	Met	Pro	Ser	Phe	Lys	Tyr	Lys	Asn	Phe	Ser	Asp	
	260					265					270					
ttg	caa	gtt	aaa	gcg	tta	ctg	aat	tta	tcc	aat	cgc	taaaaccctt				918
Leu	Gln	Val	Lys	Ala	Leu	Leu	As									

<213> Helicobacter pylori

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Glu Met Arg Asp Ser Lys Ser Gln Gly Glu Leu Val Glu Asn Gly His  
35 40 45  
Leu Ile Asp Gly Ile Gly Glu Phe Ala Asn Asn Val Pro Val Gly Trp  
50 55 60  
Ile Ala Ser Phe Met Cys Thr Ile Val Trp Ala Phe Trp Tyr Phe Phe  
65 70 75 80  
Phe Gly Tyr Pro Leu Asn Ser Phe Ser Gln Ile Gly Gln Tyr Asn Glu  
85 90 95  
Glu Val Lys Ala His Asn Gln Lys Phe Glu Ala Lys Trp Lys His Leu  
100 105 110  
Gly Gln Lys Glu Leu Val Asp Met Gly Gln Gly Ile Phe Leu Val His  
115 120 125  
Cys Ser Gln Cys His Gly Ile Thr Ala Glu Gly Leu His Gly Ser Ala  
130 135 140  
Gln Asn Leu Val Arg Trp Gly Lys Glu Glu Gly Ile Met Asp Thr Ile  
145 150 155 160  
Lys His Gly Ser Lys Gly Met Asp Tyr Leu Ala Gly Glu Met Pro Ala  
165 170 175  
Met Glu Leu Asp Glu Lys Asp Ala Lys Ala Ile Ala Ser Tyr Val Met  
180 185 190  
Ala Glu Leu Ser Ser Val Lys Lys Thr Lys Asn Pro Gln Leu Ile Asp  
195 200 205  
Lys Gly Lys Glu Leu Phe Glu Ser Met Gly Cys Thr Gly Cys His Gly  
210 215 220  
Asn Asp Gly Lys Gly Leu Gln Glu Asn Gln Val Phe Ala Ala Asp Leu  
225 230 235 240  
Thr Ala Tyr Gly Thr Glu Asn Phe Leu Arg Asn Ile Leu Thr His Gly  
245 250 255  
Lys Lys Gly Asn Ile Gly His Met Pro Ser Phe Lys Tyr Lys Asn Phe  
260 265 270  
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Phe Leu Asn Gly Leu Ala Gly Asn Leu Leu Ile Val Val Ile Leu Leu  
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tgt gtg gcc gtt ttt ttt acg ctc aaa gcg atc cat atc caa aaa gag 152

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5 10 15

atg agt aag gtt ttc cca aag ctc gct aaa gcg atc act cta gcg gca 152  
Met Ser Lys Val Phe Pro Lys Leu Ala Lys Ala Ile Thr Leu Ala Ala  
20 25 30

aaa gat ggc ggg agc gaa ccg gac acg aac gcc aaa cta cga aca gcg 200  
Lys Asp Gly Gly Ser Glu Pro Asp Thr Asn Ala Lys Leu Arg Thr Ala  
35 40 45 50

att tta aac gct aaa gcg caa aac atg cct aaa gac aat att gac gca Ile Leu Asn Ala Lys Ala Gln Asn Met Pro Lys Asp Asn Ile Asp Ala 55 60 65	248
gcg att aaa aga gcg agc agt aaa gaa ggg aat ttg agt gaa atc act Ala Ile Lys Arg Ala Ser Ser Lys Glu Gly Asn Leu Ser Glu Ile Thr 70 75 80	296
tat gaa ggt aag gcg aat ttt ggc gtg cta atc atc atg gaa tgc atg Tyr Glu Gly Lys Ala Asn Phe Gly Val Leu Ile Ile Met Glu Cys Met 85 90 95	344
act gat aac ccc acc aga acc att gcc aac ctt aaa agc tat ttc aat Thr Asp Asn Pro Thr Arg Thr Ile Ala Asn Leu Lys Ser Tyr Phe Asn 100 105 110	392
aaa acg caa ggg gca agc atc gtg cct aat ggc tct tta gag ttt atg Lys Thr Gln Gly Ala Ser Ile Val Pro Asn Gly Ser Leu Glu Phe Met 115 120 125 130	440
ttt aac cga aaa agc gtg ttt gaa tgc ttg aaa aat gaa gtg gaa aat Phe Asn Arg Lys Ser Val Phe Glu Cys Leu Lys Asn Glu Val Glu Asn 135 140 145	488
tta aaa ctc agt cta gaa gat tta gaa ttc gct ctc att gat tat ggt Leu Lys Leu Ser Leu Glu Asp Leu Glu Phe Ala Leu Ile Asp Tyr Gly 150 155 160	536
ttg gaa gaa tta gaa gaa gtg gaa gac aag atc att att agg ggg gat Leu Glu Glu Leu Glu Glu Val Glu Asp Lys Ile Ile Arg Gly Asp 165 170 175	584
tat aac agc ttc aag ctt tta aat gag ggg ttt gaa agc ttg aaa tta Tyr Asn Ser Phe Lys Leu Leu Asn Glu Gly Phe Glu Ser Leu Lys Leu 180 185 190	632
ccc att tta aaa gcg agt ttg caa cgc atc gcc aca acg ccc att gaa Pro Ile Leu Lys Ala Ser Leu Gln Arg Ile Ala Thr Thr Pro Ile Glu 195 200 205 210	680
ttg aat gac gaa caa atg gag ctt acc gaa aaa tta ctg gac agg att Leu Asn Asp Glu Gln Met Glu Leu Thr Glu Lys Leu Leu Asp Arg Ile 215 220 225	728
gaa gac gat gat gat gtg gtc gcg ctt tat acc aat att gag Glu Asp Asp Asp Asp Val Val Ala Leu Tyr Thr Asn Ile Glu 230 235 240	770
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35	40	45	
Thr Ala Ile Leu Asn Ala Lys Ala Gln Asn Met Pro Lys Asp Asn Ile			
50	55	60	
Asp Ala Ala Ile Lys Arg Ala Ser Ser Lys Glu Gly Asn Leu Ser Glu			
65	70	75	80
Ile Thr Tyr Glu Gly Lys Ala Asn Phe Gly Val Leu Ile Ile Met Glu			
85	90	95	
Cys Met Thr Asp Asn Pro Thr Arg Thr Ile Ala Asn Leu Lys Ser Tyr			
100	105	110	
Phe Asn Lys Thr Gln Gly Ala Ser Ile Val Pro Asn Gly Ser Leu Glu			
115	120	125	
Phe Met Phe Asn Arg Lys Ser Val Phe Glu Cys Leu Lys Asn Glu Val			
130	135	140	
Glu Asn Leu Lys Leu Ser Leu Glu Asp Leu Glu Phe Ala Leu Ile Asp			
145	150	155	160
Tyr Gly Leu Glu Glu Leu Glu Glu Val Glu Asp Lys Ile Ile Ile Arg			
165	170	175	
Gly Asp Tyr Asn Ser Phe Lys Leu Leu Asn Glu Gly Phe Glu Ser Leu			
180	185	190	
Lys Leu Pro Ile Leu Lys Ala Ser Leu Gln Arg Ile Ala Thr Thr Pro			
195	200	205	
Ile Glu Leu Asn Asp Glu Gln Met Glu Leu Thr Glu Lys Leu Leu Asp			
210	215	220	
Arg Ile Glu Asp Asp Asp Asp Val Val Ala Leu Tyr Thr Asn Ile Glu			
225	230	235	240

<210> 275  
 <211> 451  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (108)...(392)

<400> 275	
atcagagggga ttacgcctgg aaggataaga atttttaggga tctgtaagaa gatctagaag	60
aagcgataga atacaacaaa aagggtcagg ggcattttat aggcacc atg gtt gtc	116
Met Val Val	
1	
gct aag aat gaa gac aac aaa aaa ttg tat gac atc att gac ggc cag	164
Ala Lys Asn Glu Asp Asn Lys Lys Leu Tyr Asp Ile Ile Asp Gly Gln	
5 10 15	
caa cga acg act acc atc ttc atg ctc ttg cat gtc ttg gcg aac aaa	212
Gln Arg Thr Thr Thr Ile Phe Met Leu Leu His Val Leu Ala Asn Lys	
20 25 30 35	
caa aac gag aaa gac aag caa gaa aca aga aaa tat cta tac caa aag	260
Gln Asn Glu Lys Asp Lys Gln Glu Thr Arg Lys Tyr Leu Tyr Gln Lys	
40 45 50	
ggg gaa tta aaa tta gaa gtc gcc ccc aaa aac caa agc ttc ttc aaa	308
Gly Glu Leu Lys Leu Glu Val Ala Pro Lys Asn Gln Ser Phe Phe Lys	



50	55							60							65					
ggc tct tgc gcg atg atg gtt aat ggg aga ccg agg cta gct tgt aaa																				296
Gly Ser Cys Ala Met Met Val Asn Gly Arg Pro Arg Leu Ala Cys Lys																				
	70							75							80					
acc cta act tct agc ttt gaa agc ggg gtg atc acg ctc atg ccc atg																				344
Thr Leu Thr Ser Ser Phe Glu Ser Gly Val Ile Thr Leu Met Pro Met																				
	85							90							95					
ccc agt ttt acg ctc att aaa gat ttg agc gtg aat acg ggc gat tgg																				392
Pro Ser Phe Thr Leu Ile Lys Asp Leu Ser Val Asn Thr Gly Asp Trp																				
	100							105							110					
ttt ttg gat atg act aaa agg gtg gag agt tgg gcg cat tct aaa gaa																				440
Phe Leu Asp Met Thr Lys Arg Val Glu Ser Trp Ala His Ser Lys Glu																				
	115							120							125					
gaa gtg gat att act aga ccg gaa aaa agg gtt gag cct gac gaa gcc																				488
Glu Val Asp Ile Thr Arg Pro Glu Lys Arg Val Glu Pro Asp Glu Ala																				
	130							135							140					145
caa gaa gtc ttt gaa cta gac agg tgt att gaa tgc ggg tgt tgt atc																				536
Gln Glu Val Phe Glu Leu Asp Arg Cys Ile Glu Cys Gly Cys Cys Ile																				
	150							155							160					
gct tct tgc ggg act aaa ctc atg cgc cct aat ttc att gga gct gct																				584
Ala Ser Cys Gly Thr Lys Leu Met Arg Pro Asn Phe Ile Gly Ala Ala																				
	165							170							175					
ggc atg aac aga gcc atg cgt ttt atg att gac agc cac gat gaa aga																				632
Gly Met Asn Arg Ala Met Arg Phe Met Ile Asp Ser His Asp Glu Arg																				
	180							185							190					
aac gat gat gat ttt tat gag tta gtc ggc gat gat gat ggt gtt ttt																				680
Asn Asp Asp Asp Phe Tyr Glu Leu Val Gly Asp Asp Asp Gly Val Phe																				
	195							200							205					
ggg tgc atg agc ctt atc gct tgc cat gac act tgc cc taaagaatta																				728
Gly Cys Met Ser Leu Ile Ala Cys His Asp Thr Cys																				
	210							215							220					
cccttgcaaaa gcagtatcgc cactttgcgt aacaggatgt tgaaaagtggg taaaagccgc																				788
taattttctttt ttaagtgggtc gttttttgaaa atcttttttag tctttttaag cg																				840

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<210> 278
<211> 222
<212> PRT
<213> Helicobacter pylori
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<400> 278															
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1				5					10					15	
Pro	Gln	Ser	Ala	Val	Ser	Lys	Pro	His	Phe	Lys	Glu	Tyr	Gln	Leu	Lys
			20					25					30		
Glu	Thr	Pro	Ser	Met	Thr	Leu	Phe	Ile	Ala	Leu	Asn	Leu	Ile	Arg	Glu
		35					40					45			
His	Gln	Asp	Pro	Asp	Leu	Ser	Phe	Asp	Phe	Val	Cys	Arg	Ala	Gly	Ile
	50					55					60				

Cys Gly Ser Cys Ala Met Met Val Asn Gly Arg Pro Arg Leu Ala Cys  
65 70 75 80  
Lys Thr Leu Thr Ser Ser Phe Glu Ser Gly Val Ile Thr Leu Met Pro  
85 90 95  
Met Pro Ser Phe Thr Leu Ile Lys Asp Leu Ser Val Asn Thr Gly Asp  
100 105 110  
Trp Phe Leu Asp Met Thr Lys Arg Val Glu Ser Trp Ala His Ser Lys  
115 120 125  
Glu Glu Val Asp Ile Thr Arg Pro Glu Lys Arg Val Glu Pro Asp Glu  
130 135 140  
Ala Gln Glu Val Phe Glu Leu Asp Arg Cys Ile Glu Cys Gly Cys Cys  
145 150 155 160  
Ile Ala Ser Cys Gly Thr Lys Leu Met Arg Pro Asn Phe Ile Gly Ala  
165 170 175  
Ala Gly Met Asn Arg Ala Met Arg Phe Met Ile Asp Ser His Asp Glu  
180 185 190  
Arg Asn Asp Asp Asp Phe Tyr Glu Leu Val Gly Asp Asp Asp Gly Val  
195 200 205  
Phe Gly Cys Met Ser Leu Ile Ala Cys His Asp Thr Cys Pro  
210 215 220

<210> 279  
<211> 351  
<212> DNA  
<213> Helicobacter pylori

<220>  
<221> CDS  
<222> (53)...(262)

<400> 279  
gaaagccaaa gtagcccccctt gattgaaaca agattgagcgc atcccataag cg atg gat 58  
Met Asp  
1  
tta ttg ttc gcc acc cct aca ata agc cct ttt tta cct ttt aaa aat 106  
Leu Leu Phe Ala Thr Pro Thr Ile Ser Pro Phe Leu Pro Phe Lys Asn  
5 10 15  
ccc atg att ttc ctt tat aaa aat gaa atg att gtt tta aaa ttt tct 154  
Pro Met Ile Phe Leu Tyr Lys Asn Glu Met Ile Val Leu Lys Phe Ser  
20 25 30  
aat tcc caa gac gcg ctc ccg atc aac aag cca tcc acg cta tca atc 202  
Asn Ser Gln Asp Ala Leu Pro Ile Asn Lys Pro Ser Thr Leu Ser Ile  
35 40 45 50  
cct aaa att tct tta gcg ttt tgt gtg ttc acg ctc ccc cca tac aac 250  
Pro Lys Ile Ser Leu Ala Phe Cys Val Phe Thr Leu Pro Pro Tyr Asn  
55 60 65  
aag ggc gtt ttt tgatttaaga tttgctttaa aaaaccatgc gtgagataaa 302  
Lys Gly Val Phe  
70  
tatctttctaa agaagcgctt tttttggtgc caatcgccca aataggctc 351

<210> 280  
<211> 70



<212> PRT  
<213> Helicobacter pylori

<400> 280  
Met Asp Leu Leu Phe Ala Thr Pro Thr Ile Ser Pro Phe Leu Pro Phe  
1 5 10 15  
Lys Asn Pro Met Ile Phe Leu Tyr Lys Asn Glu Met Ile Val Leu Lys  
20 25 30  
Phe Ser Asn Ser Gln Asp Ala Leu Pro Ile Asn Lys Pro Ser Thr Leu  
35 40 45  
Ser Ile Pro Lys Ile Ser Leu Ala Phe Cys Val Phe Thr Leu Pro Pro  
50 55 60  
Tyr Asn Lys Gly Val Phe  
65 70

<210> 281  
<211> 1271  
<212> DNA  
<213> Helicobacter pylori

<220>  
<221> CDS  
<222> (368)...(1210)

<400> 281  
ttaaaggact atgcatgcaa gagattatcc ctattgtcgt ggcttttgat aacaactatt 60  
gtatccctgc tggcgtgagc ttattttcca tgctagcaaa cgccaaacga gagagagaga 120  
gagagagaga gtaaaactct tttatcaaat ccattgtttg gtggagagtt taaccccaga 180  
gaatatagcc aaattagaag aaacgatcgc tcctttttaga gctttttcta gcatagagtt 240  
tttgatatt accgataaag aattagaacc acgccacaat tataataagc ttgatccttt 300  
aatagcgagt gaaattaaaa aattgtattt aaaactcaat gctttttcgc aaaaacgctt 360  
ttctaaa atg atc atg tgc cgt ttc ttt ttt gcc tcc ctt ttc ccc caa 409  
Met Ile Met Cys Arg Phe Phe Phe Ala Ser Leu Phe Pro Gln  
1 5 10  
tac gat aag atg atc atg ttt gat gtg gac act ttg ttt gtg aat gat 457  
Tyr Asp Lys Met Ile Met Phe Asp Val Asp Thr Leu Phe Val Asn Asp  
15 20 25 30  
att agc gag agc ttt ttt atc ccc ctt gaa acg cat tat ttt ggg gct 505  
Ile Ser Glu Ser Phe Phe Ile Pro Leu Glu Thr His Tyr Phe Gly Ala  
35 40 45  
gtg agg gaa aaa gat ttg atc gct ata aat agg aat tcg gct aag gat 553  
Val Arg Glu Lys Asp Leu Ile Ala Ile Asn Arg Asn Ser Ala Lys Asp  
50 55 60  
tta tac gaa ttg cgc caa atg cat gca aaa tct atc ggc atc gcc aac 601  
Leu Tyr Glu Leu Arg Gln Met His Ala Lys Ser Ile Gly Ile Ala Asn  
65 70 75  
gct ttc cct aat tta gaa gaa gct caa atc ctt ttt gac aac tac ttt 649  
Ala Phe Pro Asn Leu Glu Glu Ala Gln Ile Leu Phe Asp Asn Tyr Phe  
80 85 90  
aac gcc ggg ttt tta gcc tta aat tta aaa tca tgg cgt aaa gaa aat 697  
Asn Ala Gly Phe Leu Ala Leu Asn Leu Lys Ser Trp Arg Lys Glu Asn  
95 100 105 110

09895913-062901

ctt	gaa	aac	caa	ttg	att	acc	ttt	ttc	att	ttg	aaa	aat	gaa	aaa	ctt	745	
Leu	Glu	Asn	Gln	Leu	Ile	Thr	Phe	Phe	Ile	Leu	Lys	Asn	Glu	Lys	Leu		
				115					120					125			
tta	ttt	aac	gat	caa	gat	gct	ttg	tgt	ttt	gtg	tgc	cgt	ggg	agg	att	793	
Leu	Phe	Asn	Asp	Gln	Asp	Ala	Leu	Cys	Phe	Val	Cys	Arg	Gly	Arg	Ile		
				130					135					140			
tta	gaa	ttg	cct	tat	cca	tac	aat	gcc	cac	cct	agt	ttc	ctt	gat	acg	841	
Leu	Glu	Leu	Pro	Tyr	Pro	Tyr	Asn	Ala	His	Pro	Ser	Phe	Leu	Asp	Thr		
				145					150					155			
ctc	tca	ttc	cct	agc	atc	aaa	gaa	gcg	cgc	atg	ctg	cat	ttt	tgg	ggc	889	
Leu	Ser	Phe	Pro	Ser	Ile	Lys	Glu	Ala	Arg	Met	Leu	His	Phe	Trp	Gly		
				160					165					170			
gat	aaa	ccc	tgg	aaa	ctc	tta	agc	gtc	att	ggc	gcg	aaa	aaa	tgg	cat	937	
Asp	Lys	Pro	Trp	Lys	Leu	Leu	Ser	Val	Ile	Gly	Ala	Lys	Lys	Trp	His		
				175					180					185			
gaa	gcg	ttg	atc	caa	acg	cct	ttt	aaa	gac	gcc	tat	ttc	aac	gct	tct	985	
Glu	Ala	Leu	Ile	Gln	Thr	Pro	Phe	Lys	Asp	Ala	Tyr	Phe	Asn	Ala	Ser		
				195					200					205			
ttt	tta	gat	cac	ctc	ttt	gaa	tcc	ctt	caa	aac	aag	gat	aat	gag	atc	1033	
Phe	Leu	Asp	His	Leu	Phe	Glu	Ser	Leu	Gln	Asn	Lys	Asp	Asn	Glu	Ile		
				210					215					220			
aaa	aga	aga	gat	gaa	agg	atc	att	gaa	gca	ctt	caa	gca	agg	gat	aaa	1081	
Lys	Arg	Arg	Asp	Glu	Arg	Ile	Ile	Glu	Ala	Leu	Gln	Ala	Arg	Asp	Lys		
				225					230					235			
atc	ctg	tct	ttt	tca	gac	aag	cga	cat	tct	ttt	gaa	tct	ctt	ctg	ccc	1129	
Ile	Leu	Ser	Phe	Ser	Asp	Lys	Arg	His	Ser	Phe	Glu	Ser	Leu	Leu	Pro		
				240					245					250			
aag	ctt	tct	tct	aaa	ctc	ctt	ata	gaa	ttt	ttg	ctt	ttt	aaa	gcc	aaa	1177	
Lys	Leu	Ser	Ser	Lys	Leu	Leu	Ile	Glu	Phe	Leu	Leu	Phe	Lys	Ala	Lys		
				255					260					265			
caa	aaa	gtg	aag	cga	ctg	att	aaa	agg	gtt	ttt	taaaaccctt				tttaaactaa		1230
Gln	Lys	Val	Lys	Arg	Leu	Ile	Lys	Arg	Val	Phe							
				275					280								
tgcgagcaag catgggtttg tgtgggctgg atgtccttat t																1271	

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<210> 282
<211> 281
<212> PRT
<213> Helicobacter pylori
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Met	Ile	Met	Cys	Arg	Phe	Phe	Phe	Ala	Ser	Leu	Phe	Pro	Gln	Tyr	Asp
1				5					10					15	
Lys	Met	Ile	Met	Phe	Asp	Val	Asp	Thr	Leu	Phe	Val	Asn	Asp	Ile	Ser
			20					25					30		
Glu	Ser	Phe	Phe	Ile	Pro	Leu	Glu	Thr	His	Tyr	Phe	Gly	Ala	Val	Arg
		35					40					45			
Glu	Lys	Asp	Leu	Ile	Ala	Ile	Asn	Arg	Asn	Ser	Ala	Lys	Asp	Leu	Tyr

09095913.062901

50	55	60
Glu Leu Arg Gln Met His Ala Lys Ser Ile Gly Ile Ala Asn Ala Phe		
65	70	75
Pro Asn Leu Glu Glu Ala Gln Ile Leu Phe Asp Asn Tyr Phe Asn Ala		80
	85	90
Gly Phe Leu Ala Leu Asn Leu Lys Ser Trp Arg Lys Glu Asn Leu Glu		95
	100	105
Asn Gln Leu Ile Thr Phe Phe Ile Leu Lys Asn Glu Lys Leu Leu Phe		110
	115	120
Asn Asp Gln Asp Ala Leu Cys Phe Val Cys Arg Gly Arg Ile Leu Glu		125
	130	135
Leu Pro Tyr Pro Tyr Asn Ala His Pro Ser Phe Leu Asp Thr Leu Ser		140
145	150	155
Phe Pro Ser Ile Lys Glu Ala Arg Met Leu His Phe Trp Gly Asp Lys		160
	165	170
Pro Trp Lys Leu Leu Ser Val Ile Gly Ala Lys Lys Trp His Glu Ala		175
	180	185
Leu Ile Gln Thr Pro Phe Lys Asp Ala Tyr Phe Asn Ala Ser Phe Leu		190
	195	200
Asp His Leu Phe Glu Ser Leu Gln Asn Lys Asp Asn Glu Ile Lys Arg		205
	210	215
Arg Asp Glu Arg Ile Ile Glu Ala Leu Gln Ala Arg Asp Lys Ile Leu		220
225	230	235
Ser Phe Ser Asp Lys Arg His Ser Phe Glu Ser Leu Leu Pro Lys Leu		240
	245	250
Ser Ser Lys Leu Leu Ile Glu Phe Leu Leu Phe Lys Ala Lys Gln Lys		255
	260	265
Val Lys Arg Leu Ile Lys Arg Val Phe		270
	275	280

<210> 283  
 <211> 1198  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (51)...(1145)

<400> 283	
atttagacaa taacgctaca actaggattg accctaaagt caaagagatc atg gat	56
	Met Asp
	1
cct ttt tta agg gat cat tat ggg aat cct agc tcg ttg cac cag ttt	104
Pro Phe Leu Arg Asp His Tyr Gly Asn Pro Ser Ser Leu His Gln Phe	
	5 10 15
ggc aca gaa acc cac cca gcc att gca gaa gcg cta gat aag ctt tat	152
Gly Thr Glu Thr His Pro Ala Ile Ala Glu Ala Leu Asp Lys Leu Tyr	
	20 25 30
aag ggc att aac gct agg gat ata gat gat gtg atc atc act tct tgt	200
Lys Gly Ile Asn Ala Arg Asp Ile Asp Asp Val Ile Ile Thr Ser Cys	
	35 40 45 50
gcg aca gaa agc aat aat tgg gtt tta aag ggc gtg tat ttt gat gaa	248
Ala Thr Glu Ser Asn Asn Trp Val Leu Lys Gly Val Tyr Phe Asp Glu	
	55 60 65

tgc Cys	ttg Leu	aaa Lys	aaa Lys 70	ggc Gly	aaa Lys	aac Asn	cat His	att Ile 75	gta Val	acc Thr	acg Thr	gtt Val	gca Ala 80	gag Glu	cat His	296
ccg Pro	gcg Ala	gtg Val 85	cga Arg	tcc Ser	act Thr	tgc Cys	aat Asn 90	ttt Phe	tta Leu	gaa Glu	agc Ser	ttg Leu 95	ggg Gly	gtg Val	gag Glu	344
gtt Val	act Thr 100	tac Tyr	ttg Leu	ccc Pro	att Ile	aat Asn 105	gag Glu	cat His	ggg Gly	agc Ser	atc Ile 110	acc Thr	gca Ala	gag Glu	caa Gln	392
gtc Val 115	aaa Lys	gaa Glu	gcg Ala	atc Ile	aca Thr 120	gaa Glu	aaa Lys	acc Thr	gct Ala	cta Leu 125	gtg Val	agc Ser	gtg Val	atg Met	tgg Trp 130	440
gcg Ala	aat Asn	aat Asn	gaa Glu 135	acc Thr	ggg Gly	ctc Leu	att Ile	ttc Phe	cct Pro 140	att Ile	gaa Glu	gaa Glu	att Ile	ggg Gly 145	gct Ala	488
att Ile	tgt Cys	aaa Lys	gaa Glu 150	aag Lys	ggc Gly	gtg Val	ttg Leu	ttc Phe 155	cat His	acc Thr	gat Asp	gcc Ala 160	gtg Val	caa Gln	gcg Ala	536
att Ile	ggg Gly 165	aaa Lys	atc Ile	cct Pro	gta Val	gat Asp	gtg Val 170	tta Leu	aaa Lys	gcg Ala	aat Asn	gca Ala 175	gat Asp	ttc Phe	ctt Leu	584
tct Ser	ttt Phe 180	agc Ser	gcg Ala	cac His	aag Lys	ttt Phe 185	cat His	ggg Gly	cct Pro	aaa Lys	ggc Gly 190	att Ile	ggg Gly	ggg Gly	ttg Leu	632
tat Tyr 195	att Ile	aga Arg	agt Ser	ggg Gly 200	gtg Val	gga Gly	ttg Leu	acc Thr	cct Pro	ctt Leu 205	ttt Phe	cat His	ggc Gly	ggg Gly	gag Glu 210	680
cat His	atg Met	aat Asn	ggc Gly 215	agg Arg	cgc Arg	agc Ser	ggg Gly	act Thr 220	ttg Leu	aat Asn	gtg Val	cct Pro	tat Tyr	att Ile 225	gtg Val	728
gga Gly	atg Met	ggc Gly	gaa Glu 230	gcg Ala	atg Met	aaa Lys	tta Leu	gcc Ala 235	gta Val	gag Glu	cat His	tta Leu	gac Asp 240	tat Tyr	gaa Glu	776
aaa Lys	gaa Glu	gtg Val 245	gtg Val	ggg Gly	aaa Lys	ttg Leu	cgc Arg 250	gac Asp	aaa Lys	tta Leu	gaa Glu	gaa Glu 255	gcg Ala	ctt Leu	ttg Leu	824
aaa Lys	atc Ile 260	cct Pro	gat Asp	gtg Val	atg Met	gtg Val 265	gtg Val	ggc Gly	gat Asp	aga Arg	atc Ile 270	cat His	cgt Arg	gtg Val	cct Pro	872
aac Asn 275	acg Thr	act Thr	tta Leu	gtc Val	agc Ser 280	gtg Val	aga Arg	ggg Gly	att Ile	gaa Glu 285	gga Gly	gag Glu	gcc Ala	atg Met	ctg Leu 290	920
tgg Trp	gat Asp	tta Leu	aac Asn	cgc Arg	tct Ser	aat Asn	atc Ile	gcc Ala	gct Ala	tcc Ser	aca Thr	ggg Gly	agc Ser	gcg Ala	tgc Cys	968





gcg Ala	cta Leu	ggc Gly	att Ile	ttg Leu 135	ctt Leu	tta Leu	atg Met	gag Glu	caa Gln 140	ttc Phe	aaa Lys	ttc Phe	ctt Leu	caa Gln 145	aac Asn	488
caa Gln	aat Asn	ttg Leu	ggg Gly 150	gtg Val	ttt Phe	gtc Val	ttg Leu	ctc Leu 155	gct Ala	att Ile	ggg Gly	ata Ile	ctc Leu 160	atc Ile	att Ile	536
tat Tyr	ctt Leu	ttt Phe 165	cct Pro	cta Leu	atc Ile	act Thr	aaa Lys 170	aaa Lys	atc Ile	ccc Pro	tct Ser	aat Asn 175	ctg Leu	att Ile	tgt Cys	584
atc Ile 180	ctt Leu	ata Ile	gtg Val	agc Ser	gcg Ala	atc Ile 185	gct Ala	tta Leu	att Ile	ttt Phe	gat Asp 190	atg Met	cat His	gcg Ala	ccg Pro	632
aat Asn 195	ttg Leu	ggg Gly	agc Ser	att Ile	gag Glu 200	caa Gln	ggg Gly	gtt Val	tca Ser	ggc Gly 205	ttt Phe	cat His	ttc Phe	atc Ile	att Ile 210	680
atc Ile	ccc Pro	aaa Lys	aat Asn	ttg Leu 215	gat Asp	ttt Phe	aaa Lys	ata Ile	atg Met 220	ata Ile	gag Glu	ttg Leu	ttg Leu	cct Pro 225	tac Tyr	728
gct Ala	ctt Leu	tct Ser	tta Leu 230	gca Ala	cta Leu	gtg Val	gga Gly	acg Thr 235	ata Ile	gaa Glu	agc Ser	tta Leu	ttg Leu 240	acg Thr	gct Ala	776
aaa Lys	act Thr	tta Leu 245	gat Asp	gtg Val	att Ile	tta Leu	aaa Lys 250	gac Asp	ggc Gly	gtg Val	agc Ser	gat Asp 255	aaa Lys	aat Asn	aaa Lys	824
gaa Glu	act Thr 260	aaa Lys	gcg Ala	caa Gln	ggc Gly	ttg Leu 265	ggg Gly	aat Asn	atc Ile	atc Ile	tca Ser 270	ggg Gly	ctt Leu	ttg Leu	ggg Gly	872
gga Gly 275	atg Met	aca Thr	ggg Gly	tgc Cys	gct Ala 280	tta Leu	gtg Val	ggg Gly	cag Gln	tct Ser 285	atc Ile	att Ile	aac Asn	gca Ala	aaa Lys 290	920
tcc Ser	ggg Gly	gct Ala	aaa Lys	aca Thr 295	agg Arg	ctt Leu	tct Ser	act Thr	ttt Phe 300	ttt Phe	gcc Ala	ggc Gly	ttt Phe	tct Ser 305	tta Leu	968
atg Met	gtg Val	ctc Leu	ata Ile 310	tta Leu	gtg Val	ttt Phe	aat Asn	gaa Glu 315	tat Tyr	gtg Val	gtt Val	aag Lys	atc Ile 320	ccc Pro	att Ile	1016
gtg Val	gcg Ala	gtt Val 325	gtg Val	gcg Ala	gta Val	atg Met	gtg Val 330	atg Met	att Ile	tct Ser	ttc Phe	acc Thr 335	act Thr	ttt Phe	aat Asn	1064
ttc Phe 340	caa Gln	tcc Ser	att Ile	att Ile	aac Asn	att Ile 345	aaa Lys	aaa Lys	atc Ile	aag Lys	ctc Leu 350	tat Tyr	gac Asp	acg Thr	ctc Leu	1112
aac Asn	atg Met	ctc Leu	tta Leu	gtc Val	gtg Val	gcg Ala	gtg Val	gtt Val	tta Leu	tac Tyr	acg Thr	cat His	aat Asn	tta Leu	gcg Ala	1160

355                      360                      365                      370

ata ggg gtt gtg gtg ggg gtt tta gtc aat gcg tta tgg atc aaa tct      1208  
 Ile Gly Val Val Val Gly Val Leu Val Asn Ala Leu Trp Ile Lys Ser  
                                  375                                   380                                   385

aaa ggg att gca tgaaatttta ttttaaaaag ttgggtagct agagatatgg      1260  
 Lys Gly Ile Ala  
                                  390

ctccagatgt agg      1273

<210> 286  
 <211> 390  
 <212> PRT  
 <213> Helicobacter pylori

<400> 286

Met	Arg	Lys	Lys	Gly	Met	Phe	Glu	Lys	Ile	Gln	Lys	Glu	Trp	Leu	Ser
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Asn	Ile	Gln	Lys	Asp	Leu	Leu	Ser	Gly	Phe	Val	Val	Gly	Leu	Ser	Val
			20					25					30		
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Ala	Thr	Leu	Met	Ala	Gly	Val	Leu	Gln	Ile	Leu	Leu	Gly	Tyr	Leu	Lys
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Leu	Gly	Gly	Met	Thr	Gly	Cys	Ala	Leu	Val	Gly	Gln	Ser	Ile	Ile	Asn
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09095913-062901





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Glu Val Ile Thr Lys Glu Lys Gln Gly Asp Lys Thr Lys Ala Phe Asp  
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tta gtt caa gag ctt tta gaa gaa ttt ttg caa agc ggg gct aaa gag 940  
Leu Val Gln Glu Leu Leu Glu Glu Phe Leu Gln Ser Gly Ala Lys Glu  
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att tta gaa aag gcg cag ttg ttt taatgcgttt gtttatcgcg ctagttttgt 994  
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Asp Ala Ile Ile Leu Ala Glu Ala Gly Leu Cys Arg Leu Glu Ile Gln  
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Met Gly Gln Gly Ala Leu Gly Val Glu Met Leu Lys Asn His Lys His  
85 90 95  
Phe Ala Thr Leu Gln Lys Leu Asn Asp Glu Lys Ser Ala Phe Cys Cys  
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Arg Leu Glu Arg Glu Phe Ile Lys Gly Leu Asn Gly Gly Cys Gln Ile  
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130 135 140  
Ala Val Leu Gly Leu Pro Asn Gly Lys Glu Val Ile Thr Lys Glu Lys  
145 150 155 160  
Gln Gly Asp Lys Thr Lys Ala Phe Asp Leu Val Gln Glu Leu Leu Glu  
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Phe

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      20          25          30
Glu  Met  Asp  Gly  Gln  Leu  Leu  Val  Thr  Phe  Asn  Glu  Ile  Ser  Gly  Asn
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Gly	Val	Lys	His	Ser	Leu	His	Leu	Met	Pro	Ser	Gly	Val	Leu	Tyr	Pro	
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Lys	Cys	Lys	Asn	Ile	Ile	Ser	Ser	Ala	Val	Val	Val	Ser	Val	Lys	Asp	
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Leu	Cys	Glu	Glu	Ile	Ser	Ala	Phe	Glu	Asp	Leu	Glu	Asn	Arg	Leu	Phe	
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gtc	agc	gac	aga	gcc	cat	gtg	atc	ttg	ccc	tat	cat	gcc	aaa	aaa	gac	399
Val	Ser	Asp	Arg	Ala	His	Val	Ile	Leu	Pro	Tyr	His	Ala	Lys	Lys	Asp	
				95				100				105				
gct	ttt	aaa	gaa	aaa	tct	caa	aac	atc	ggc	acg	act	aaa	aaa	ggc	ata	447
Ala	Phe	Lys	Glu	Lys	Ser	Gln	Asn	Ile	Gly	Thr	Thr	Lys	Lys	Gly	Ile	
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Gly	Pro	Cys	Tyr	Glu	Asp	Lys	Met	Ala	Arg	Ser	Gly	Ile	Arg	Met	Gly	
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Asp	Leu	Leu	Asp	Asp	Lys	Ile	Leu	Glu	Glu	Lys	Leu	Asn	Ala	His	Phe	
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Lys	Ala	Ile	Glu	Pro	Phe	Lys	Lys	Ala	Tyr	Asp	Leu	Gly	Glu	Asn	Tyr	
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Glu	Lys	Asp	Leu	Met	Gly	Tyr	Phe	Lys	Thr	Tyr	Ala	Pro	Lys	Ile	Cys	
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ccc	ttt	atc	aaa	gac	acg	aca	agc	atg	ctg	ata	gaa	gcg	aat	caa	aag	687
Pro	Phe	Ile	Lys	Asp	Thr	Thr	Ser	Met	Leu	Ile	Glu	Ala	Asn	Gln	Lys	
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Gly	Glu	Lys	Ile	Leu	Leu	Glu	Gly	Ala	Gln	Gly	Thr	Leu	Leu	Asp	Ile	
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Asp	Leu	Gly	Thr	Tyr	Pro	Phe	Val	Thr	Ser	Ser	Asn	Thr	Thr	Ser	Ala	
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agc	gca	tgc	gtg	agc	acc	ggc	tta	aac	cct	aaa	gcg	atc	aat	gaa	gtc	831
Ser	Ala	Cys	Val	Ser	Thr	Gly	Leu	Asn	Pro	Lys	Ala	Ile	Asn	Glu	Val	
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Gln	Gly	Gly 35	His	Asn	Ala	Gly	His 40	Thr	Ile	Val	His 45	Lys	Gly	Val	Lys
His	Ser 50	Leu	His	Leu	Met	Pro 55	Ser	Gly	Val	Leu	Tyr 60	Pro	Lys	Cys	Lys
Asn 65	Ile	Ile	Ser	Ser	Ala 70	Val	Val	Val	Ser	Val 75	Lys	Asp	Leu	Cys	Glu 80
Glu	Ile	Ser	Ala	Phe 85	Glu	Asp	Leu	Glu	Asn 90	Arg	Leu	Phe	Val	Ser 95	Asp



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Ala Thr Phe Leu Gln Val Arg Val Gln Gly Glu Val Ser Asn Leu Thr	
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Ile His Lys Val Ser Gly His Ala Tyr Phe Ser Leu Lys Asp Ser Gln	
35 40 45 50	
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Ser Val Ile Lys Cys Val Leu Phe Lys Gly Asn Ala Asn Arg Leu Lys	
55 60 65	
ttc gct tta aaa gaa ggg cag gaa gtg gtt gtt ttt ggg ggt att agc	296
Phe Ala Leu Lys Glu Gly Gln Glu Val Val Phe Gly Gly Ile Ser	
70 75 80	
gtg tat gtc cca agg ggg gat tat caa atc aat tgc ttt gaa ata gag	344
Val Tyr Val Pro Arg Gly Asp Tyr Gln Ile Asn Cys Phe Glu Ile Glu	
85 90 95	
cct aag gat ata ggt tca tta act tta gct tta gag caa ttg aaa gaa	392
Pro Lys Asp Ile Gly Ser Leu Thr Leu Ala Leu Glu Gln Leu Lys Glu	
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180 185 190	
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Asp Leu Tyr Ser Phe Asn Asp Glu Lys Ile Ala Asp Ala Leu Tyr Leu	
215 220 225	
gcc aaa acc ttc agc atg tca gct att ggg cat gag agc gat ttt tta	776
Ala Lys Thr Phe Ser Met Ser Ala Ile Gly His Glu Ser Asp Phe Leu	
230 235 240	
ttg agc gat tta gtg gcg gat tta agg gct tct acg cct tca aac gcg	824
Leu Ser Asp Leu Val Ala Asp Leu Arg Ala Ser Thr Pro Ser Asn Ala	
245 250 255	





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Thr Lys Asn Ala Phe Asp Ala Ile Val Val Ala Arg Gly Gly Gly Ser  
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Ile Lys Asn Asp Arg Ile Lys Glu Lys Phe Phe Lys Thr Phe Glu Thr		
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Lys Val Glu Thr Lys Asn Gly Glu Val Pro Ile Gln Ala Leu Lys Ile		
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Ala Arg Thr Tyr Ser Gln Lys Tyr Pro Tyr Thr Tyr Phe Ser Ala Met		
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Ile Gly Leu Asp Ser Ser Lys Asp Asn Ser Glu Lys Ile Thr Glu Asp	
230 235 240	
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Ala Tyr Ser Leu Ile Glu Gly Met Thr Asn Ile Pro Leu Ile Ala Asp	
245 250 255	
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Val Leu Gln Glu Gly Leu Arg Gly Val Tyr His Ser Arg Glu Ile Asp	
260 265 270	
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Phe Val Glu Lys Val Val Val Leu Asp Ser Cys Gln Ile His Gln Lys	
275 280 285 290	
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Ala Leu Met His Leu Gln Glu Thr Leu Met Ile Glu Val Asp Arg Leu	
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Asp Phe Ser Leu Val Glu Arg Leu Asn Ile Leu Ala Arg Met Glu Asn	
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Arg Phe Lys Ile Gln Asp Val Asp Phe Leu Phe Ser Pro Phe Ser Leu	
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145 150 155 160	
Leu Leu Leu Glu Arg Ser Arg Phe Tyr Phe Leu Ile Ala Asp Lys Lys	
165 170 175	



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Ser Leu Ser Asp Asn Val Lys Leu Gln Glu Asp Gly Ile Val Phe Lys	
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Ser His Ile Asp Gly Ser Lys His Leu Phe Thr Pro Ala Lys Val Leu	
115 120 125	
gac att caa tat tct ttg aat agc gat att atg atg gtt tta gac gat	492
Asp Ile Gln Tyr Ser Leu Asn Ser Asp Ile Met Met Val Leu Asp Asp	
130 135 140 145	
tta gtg ggc ttg ccc gct ccc tta aaa cgc ctt gaa gaa tcc att aaa	540
Leu Val Gly Leu Pro Ala Pro Leu Lys Arg Leu Glu Glu Ser Ile Lys	
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aga agt gct aaa tgg gcg aat atg agc cta gaa tac cac aaa gaa aaa	588
Arg Ser Ala Lys Trp Ala Asn Met Ser Leu Glu Tyr His Lys Glu Lys	
165 170 175	
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Asn Arg Pro Ser Asn Asn Leu Phe Ala Ile Ile Gln Gly Gly Thr His	
180 185 190	
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195 200 205	
ggc tac gct ata ggc ggt tta gcg gtg ggg gaa agc gct gat gaa atg	732
Gly Tyr Ala Ile Gly Gly Leu Ala Val Gly Glu Ser Ala Asp Glu Met	
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Arg Tyr Leu Met Gly Val Gly Thr Pro Glu Asn Ile Leu Asp Ala Ile	
245 250 255	
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Ser Leu Gly Val Asp Met Phe Asp Cys Val Met Pro Thr Arg Asn Ala	
260 265 270	
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Arg Asn Ala Thr Leu Phe Thr His Ser Gly Lys Ile Ser Ile Lys Asn	
275 280 285	
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Ala Pro Tyr Lys Leu Asp Asn Thr Pro Ile Glu Glu Asn Cys Ala Cys	
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Tyr Ala Cys Lys Arg Tyr Ser Lys Ala Tyr Leu His His Leu Phe Arg	
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Ala Lys Glu Leu Thr Tyr Ala Arg Leu Ala Ser Leu His Asn Leu His	
325 330 335	

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340 345 350

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Gly Thr Gln Gly Cys Ile Lys Ser Leu Asp Ala Thr Asp Ala Gln Glu  
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Ala Gln Phe Tyr Gly Ser Phe Leu Thr Asp Ser Gly Gly Phe Gln Ala  
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Lys Arg Ser Ala Lys Trp Ala Asn Met Ser Leu Glu Tyr His Lys Glu  
165 170 175  
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210 215 220  
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225 230 235 240  
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245 250 255  
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260 265 270  
Ala Arg Asn Ala Thr Leu Phe Thr His Ser Gly Lys Ile Ser Ile Lys  
275 280 285  
Asn Ala Pro Tyr Lys Leu Asp Asn Thr Pro Ile Glu Glu Asn Cys Ala  
290 295 300

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Cys Tyr Ala Cys Lys Arg Tyr Ser Lys Ala Tyr Leu His His Leu Phe  
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 caa gtg atg agc gag aat ttg aag gac ttt agc acg acc tta gaa gaa 152  
 Gln Val Met Ser Glu Asn Leu Lys Asp Phe Ser Thr Thr Leu Glu Glu  
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 Gln Glu Ala Asp Ile Ile Ile Ile Asn Ser Cys Thr Val Thr Asn Gly  
 35 40 45 50  
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 Lys Glu Val Leu Phe Thr Gly Cys Gly Val Lys Thr Gln Gly Lys Glu  
 70 75 80  
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 Leu Phe Glu Lys Gly Phe Leu Lys Gly Val Phe Gly His Asp Asn Lys  
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 Glu Lys Ile Asn Ala Leu Leu Gln Glu Lys Lys Arg Phe Phe Ile Asp  
 100 105 110  
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106290" E F 56860

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Phe	Glu	Glu	Arg	Lys	Ile	Leu	Glu	Gln	Val	Gly	Leu	Leu	Cys	Ser	Lys					
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Ile	Asn	Asp	Glu	Phe	Leu	Glu	Leu	Leu	Glu	Glu	Asp	Phe	Leu	Glu	Lys					
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Ser	Leu	Pro	Leu	Thr	His	Ile	His	Pro	Phe	Ile	Tyr	Ser	Lys	Arg	Lys					
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Ala	Phe	Arg	Gln	Leu	Gln	Leu	Lys	Leu	Asn	Thr	Pro	Leu	Lys	Ala	Leu					
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Arg Lys Asp Thr Pro Ser Ser Leu Met Thr Asp Ser Val Ser Leu Glu  
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 340 345 350  
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 355 360 365  
 Ala Leu Val Glu Val Gln Lys Asp Gly Glu Phe Lys Ala Leu Asp Gln  
 370 375 380  
 Phe Phe Asn Pro Ile Lys Ile Lys Ser Asp Lys Pro Leu Arg Ala Ser  
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 Lys Phe Gly Leu Gly Val Tyr Leu Leu Leu Gly Ile Leu Gly Gly  
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 tct ttg atc att cta gga gcg ata gtc gcg ccc att gtt ttc aaa gct 152  
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 35 40 45 50  
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 55 60 65  
 ggt ttt gta gtg tta ctt tat gaa atc att tcg ttt att tat tac aaa 296  
 Gly Phe Val Val Leu Leu Tyr Glu Ile Ile Ser Phe Ile Tyr Tyr Lys  
 70 75 80  
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 Arg Ser Leu Val Tyr Leu Ile Leu Gly Val Ala Ile Gly Ala Leu Cys  
 85 90 95  
 ttg ctc ttt gtt ttt tat tac acg cct tat att tta aac gct caa aaa 392  
 Leu Leu Phe Val Phe Tyr Tyr Thr Pro Tyr Ile Leu Asn Ala Gln Lys  
 100 105 110  
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Gly	Lys 50	Leu	Met	Ala	Gln	Ile 55	Phe	Val	Arg	Phe	Asn 60	Tyr	Val	Leu	Gly
Ala 65	Ile	Gly	Phe	Val	Val 70	Leu	Leu	Tyr	Glu	Ile 75	Ile	Ser	Phe	Ile 80	Tyr
Tyr	Lys	Arg	Ser	Leu 85	Val	Tyr	Leu	Ile	Leu 90	Gly	Val	Ala	Ile 95	Gly	Ala
Leu	Cys	Leu	Leu 100	Phe	Val	Phe	Tyr	Tyr 105	Thr	Pro	Tyr	Ile	Leu 110	Asn	Ala
Gln	Lys	Ala	Gly	Glu	Ala	Ala	Leu 120	Gln	Ser	Ala	Glu	Phe 125	Ala	Arg	Ser
His	Ala 130	Gln	Ser	Glu	Trp	Leu 135	Phe	Lys	Glu	Leu	Phe 140	Val	Leu	Val	Cys
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gaa Glu	aaa Lys	cgc Arg	cct Pro	agg Arg 295	ggg Gly	gtg Val	tat Tyr	tgc Cys	ggg Gly 300	gcg Ala	ata Ile	ggc Gly	atg Met	gtt Val 305	gaa Glu	968
gaa Glu	aaa Lys	aaa Lys	gcc Ala 310	ctt Leu	ttt Phe	agc Ser	gtg Val	cct Pro 315	atc Ile	cgc Arg	act Thr	tta Leu	gaa Glu 320	aaa Lys	aga Arg	1016
gtg Val	cac His	gaa Glu 325	aat Asn	ttt Phe	ttg Leu	cat His	tta Leu 330	ggg Gly	gta Val	ggg Gly	agt Ser	ggg Gly 335	gta Val	act Thr	tat Tyr	1064
aaa Lys	agt Ser 340	aaa Lys	gcg Ala	cca Pro	aaa Lys	gaa Glu 345	tat Tyr	gaa Glu	gaa Glu	agc Ser	ttt Phe 350	ttg Leu	aaa Lys	tcc Ser	ttt Phe	1112
ttt Phe 355	gtg Val	atg Met	ccc Pro	aaa Lys	ata Ile 360	gaa Glu	ttt Phe	gag Glu	att Ile	gta Val 365	gaa Glu	acg Thr	atg Met	aaa Lys	att Ile 370	1160
atc Ile	aaa Lys	aag Lys	gat Asp	caa Gln 375	aaa Lys	tta Leu	gag Glu	att Ile	aat Asn 380	aat Asn	aaa Lys	aac Asn	gcc Ala	cat His 385	aaa Lys	1208
gaa Glu	cgc Arg	tta Leu	atg Met 390	aat Asn	agc Ser	act Thr	cga Arg	tat Tyr 395	ttt Phe	aac Asn	ttt Phe	aaa Lys	tac Tyr 400	gat Asp	gaa Glu	1256
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ctc Leu	aat Asn 420	aaa Lys	aag Lys	ggc Gly	aag Lys	ctc Leu 425	att Ile	aaa Lys	gaa Glu	tac Tyr	aaa Lys 430	acc Thr	tta Leu	gag Glu	cct Pro	1352
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aat Asn	gat Asp	ttt Phe	tta Leu	tac Tyr 455	cat His	aag Lys	acc Thr	act Thr	tat Tyr 460	gcc Ala	cct Pro	ttt Phe	tat Tyr	caa Gln 465	aag Lys	1448
gct Ala	cga Arg	gcg Ala	ctc Leu 470	att Ile	aaa Lys	aag Lys	ggc Gly	gtt Val 475	atg Met	ttt Phe	gat Asp	gaa Glu	atc Ile	ttt Phe	tat Tyr	1496
aac Asn	cag Gln	gat Asp 485	ttg Leu	gaa Glu	ctc Leu	act Thr	gag Glu 490	ggc Gly	gct Ala	agg Arg	agc Ser	aat Asn 495	ctt Leu	gtt Val	tta Leu	1544



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Ser Leu Glu Lys Arg Pro	Arg Gly Val Tyr Cys Gly	Ala Ile Gly Met
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Lys Arg Val His Glu Asn	Phe Leu His Leu Gly	Val Gly Ser Gly Val
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Thr Tyr Lys Ser Lys Ala	Pro Lys Glu Tyr Glu	Glu Ser Phe Leu Lys
340	345	350
Ser Phe Phe Val Met Pro	Lys Ile Glu Phe Glu	Ile Val Glu Thr Met
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Lys Ile Ile Lys Lys Asp	Gln Lys Leu Glu Ile	Asn Asn Lys Asn Ala
370	375	380
His Lys Glu Arg Leu Met	Asn Ser Thr Arg Tyr	Phe Asn Phe Lys Tyr
385	390	395
Asp Glu Asn Leu Leu Asp	Phe Glu Leu Glu Lys	Glu Gly Val Leu Arg
405	410	415
Val Leu Leu Asn Lys Lys	Gly Lys Leu Ile Lys	Glu Tyr Lys Thr Leu
420	425	430
Glu Pro Leu Lys Ser Leu	Glu Ile Arg Leu Ser	Glu Ala Pro Ile Asp
435	440	445
Lys Arg Asn Asp Phe Leu	Tyr His Lys Thr Thr	Tyr Ala Pro Phe Tyr
450	455	460
Gln Lys Ala Arg Ala Leu	Ile Lys Lys Gly Val	Met Phe Asp Glu Ile
465	470	475
Phe Tyr Asn Gln Asp Leu	Glu Leu Thr Glu Gly	Ala Arg Ser Asn Leu
485	490	495
Val Leu Glu Ile His Asn	Arg Leu Leu Thr Pro	Tyr Phe Ser Ala Gly
500	505	510
Ala Leu Asn Gly Thr Gly	Val Val Gly Leu Leu	Lys Lys Gly Leu Val
515	520	525
Gly His Ala Pro Leu Lys	Leu Gln Asp Leu Gln	Lys Ala Ser Lys Ile
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Ser Phe Arg Glu Phe Ile Gln Gln Phe Lys Lys Asn Lys Ala Ala Val	
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Val Gly Ala Trp Ile Val Leu Leu Val Ile Cys Ala Ile Phe Ala	
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Leu	Leu	Lys	Pro	Ile	Trp	Glu	His	Gly	Gly	Asn	Ala	Lys	Tyr	Leu	Leu	
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Gly	Thr	Asp	Asp	Leu	Gly	Arg	Asp	Ile	Leu	Ser	Arg	Leu	Ile	Tyr	Gly	
			70				75						80			
gcc	agg	att	tct	tta	acc	ata	ggg	att	gtt	tct	atg	ggg	att	gcg	gtg	344
Ala	Arg	Ile	Ser	Leu	Thr	Ile	Gly	Ile	Val	Ser	Met	Gly	Ile	Ala	Val	
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Phe	Phe	Gly	Thr	Ile	Leu	Gly	Leu	Ile	Ala	Gly	Tyr	Phe	Gly	Gly	Lys	
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aca	gat	gca	att	atc	atg	cgt	atc	atg	gac	atc	atg	ttc	gct	ttg	ccc	440
Thr	Asp	Ala	Ile	Ile	Met	Arg	Ile	Met	Asp	Ile	Met	Phe	Ala	Leu	Pro	
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Ser	Ile	Leu	Leu	Ile	Val	Ile	Val	Val	Ala	Val	Leu	Gly	Pro	Ser	Leu	
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Arg	Leu	Val	Arg	Ser	Ser	Val	Leu	Gly	Glu	Lys	Glu	Lys	Glu	Tyr	Val	
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Val	Ile	Phe	Pro	Asn	Cys	Ile	Ile	Pro	Leu	Ile	Val	Gln	Thr	Thr	Met	
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Gly	Phe	Ala	Ser	Thr	Val	Leu	Glu	Ala	Ala	Ala	Leu	Ser	Phe	Leu	Gly	
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ctt	ggg	gcc	caa	cct	ccc	aaa	ccc	gaa	tgg	gga	gcg	atg	ttg	atg	aat	776
Leu	Gly	Ala	Gln	Pro	Pro	Lys	Pro	Glu	Trp	Gly	Ala	Met	Leu	Met	Asn	
			230						235					240		
tcc	atg	caa	tac	atc	gct	acc	gct	cct	tgg	atg	ctt	gtt	ttc	cct	ggg	824
Ser	Met	Gln	Tyr	Ile	Ala	Thr	Ala	Pro	Trp	Met	Leu	Val	Phe	Pro	Gly	
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gtg	atg	att	ttt	tta	acg	gtc	atg	agt	ttt	aat	ctg	gta	ggc	gat	ggc	872
Val	Met	Ile	Phe	Leu	Thr	Val	Met	Ser	Phe	Asn	Leu	Val	Gly	Asp	Gly	
		260				265					270					



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 Ile Met Asp Ala Leu Asp Pro Lys Arg Thr Ser  
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 35 40 45  
 Asp Arg Leu Leu Lys Pro Ile Trp Glu His Gly Gly Asn Ala Lys Tyr  
 50 55 60  
 Leu Leu Gly Thr Asp Asp Leu Gly Arg Asp Ile Leu Ser Arg Leu Ile  
 65 70 75 80  
 Tyr Gly Ala Arg Ile Ser Leu Thr Ile Gly Ile Val Ser Met Gly Ile  
 85 90 95  
 Ala Val Phe Phe Gly Thr Ile Leu Gly Leu Ile Ala Gly Tyr Phe Gly  
 100 105 110  
 Gly Lys Thr Asp Ala Ile Ile Met Arg Ile Met Asp Ile Met Phe Ala  
 115 120 125  
 Leu Pro Ser Ile Leu Leu Ile Val Ile Val Ala Val Leu Gly Pro  
 130 135 140  
 Ser Leu Thr Asn Ala Met Leu Ala Ile Gly Phe Val Gly Ile Pro Gly  
 145 150 155 160  
 Phe Ala Arg Leu Val Arg Ser Ser Val Leu Gly Glu Lys Glu Lys Glu  
 165 170 175  
 Tyr Val Ile Ala Ser Lys Ile Asn Gly Ser Ser His Leu Arg Leu Met  
 180 185 190  
 Cys Lys Val Ile Phe Pro Asn Cys Ile Ile Pro Leu Ile Val Gln Thr  
 195 200 205  
 Thr Met Gly Phe Ala Ser Thr Val Leu Glu Ala Ala Leu Ser Phe  
 210 215 220  
 Leu Gly Leu Gly Ala Gln Pro Pro Lys Pro Glu Trp Gly Ala Met Leu  
 225 230 235 240  
 Met Asn Ser Met Gln Tyr Ile Ala Thr Ala Pro Trp Met Leu Val Phe  
 245 250 255  
 Pro Gly Val Met Ile Phe Leu Thr Val Met Ser Phe Asn Leu Val Gly  
 260 265 270  
 Asp Gly Ile Met Asp Ala Leu Asp Pro Lys Arg Thr Ser  
 275 280 285

<210> 307  
 <211> 791  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (95)...(727)

<400> 307

00665913-0665901

0985913 "062901"

ccttggttaaa aatgtagt ggtgcaagct tgctgacaca cgccttaata gctaaagaag	60
aaagcgcagc ncttcttgga caaaaaatgt gtat atg gga gtc aat tac caa aca	115
Met Gly Val Asn Tyr Gln Thr	
1 5	
ggt tct atc aat tta atg act aat atc cat gaa gtt aga gaa gtt act	163
Gly Ser Ile Asn Leu Met Thr Asn Ile His Glu Val Arg Glu Val Thr	
10 15 20	
aac tat caa acc ggt tac acc aat att ata act agc gtt aat agc gtt	211
Asn Tyr Gln Thr Gly Tyr Thr Asn Ile Ile Thr Ser Val Asn Ser Val	
25 30 35	
aaa aag ctc acc aac atg gga tct aat ggg att gga tta gtc atg ggt	259
Lys Lys Leu Thr Asn Met Gly Ser Asn Gly Ile Gly Leu Val Met Gly	
40 45 50 55	
tat aac cac ttt ttc cat ccg gat aaa atc ttg ggc ttg cgc tat ttc	307
Tyr Asn His Phe Phe His Pro Asp Lys Ile Leu Gly Leu Arg Tyr Phe	
60 65 70	
gct ttt tta gat tgg caa ggc tat ggc atg aga tac cct aaa ggc tat	355
Ala Phe Leu Asp Trp Gln Gly Tyr Gly Met Arg Tyr Pro Lys Gly Tyr	
75 80 85	
tat ggc ggc aat aac atg atc act tat ggc gtg ggc gtg gat gca gtg	403
Tyr Gly Gly Asn Asn Met Ile Thr Tyr Gly Val Gly Val Asp Ala Val	
90 95 100	
tgg aat ttc ttt caa ggg agt ttc tat caa gat gac att agc gtg gat	451
Trp Asn Phe Phe Gln Gly Ser Phe Tyr Gln Asp Asp Ile Ser Val Asp	
105 110 115	
att ggc gtt ttt ggg ggg att gcg att gcg ggg aat agc tgg tat att	499
Ile Gly Val Phe Gly Gly Ile Ala Ile Ala Gly Asn Ser Trp Tyr Ile	
120 125 130 135	
ggc agt aaa ggg cag gaa ttg tta ggt atc act aac agc agc gcg gtt	547
Gly Ser Lys Gly Gln Glu Leu Leu Gly Ile Thr Asn Ser Ser Ala Val	
140 145 150	
gat aac acc tct ttt caa ttc ctc ttt aac ttt ggc ctc aag gct tta	595
Asp Asn Thr Ser Phe Gln Phe Leu Phe Asn Phe Gly Leu Lys Ala Leu	
155 160 165	
ttt gta gat gag cat gaa ttt gaa atc ggt ttt aaa ttc ccc acc att	643
Phe Val Asp Glu His Glu Phe Glu Ile Gly Phe Lys Phe Pro Thr Ile	
170 175 180	
aat aac aaa tac tac acc act gac gcg ctc aag gtt caa atg cgt agg	691
Asn Asn Lys Tyr Tyr Thr Thr Asp Ala Leu Lys Val Gln Met Arg Arg	
185 190 195	
gtc ttt gcc ttt tat gtg ggg tat aat tac cac ttc taaagggctt	737
Val Phe Ala Phe Tyr Val Gly Tyr Asn Tyr His Phe	
200 205 210	
ttaaaaccca acgcaactcc ctaacatctt ttggtaatag ctcttggctt tgag	791

<210> 308  
 <211> 211  
 <212> PRT  
 <213> Helicobacter pylori

<400> 308  
 Met Gly Val Asn Tyr Gln Thr Gly Ser Ile Asn Leu Met Thr Asn Ile  
 1 5 10 15  
 His Glu Val Arg Glu Val Thr Asn Tyr Gln Thr Gly Tyr Thr Asn Ile  
 20 25 30  
 Ile Thr Ser Val Asn Ser Val Lys Lys Leu Thr Asn Met Gly Ser Asn  
 35 40 45  
 Gly Ile Gly Leu Val Met Gly Tyr Asn His Phe Phe His Pro Asp Lys  
 50 55 60  
 Ile Leu Gly Leu Arg Tyr Phe Ala Phe Leu Asp Trp Gln Gly Tyr Gly  
 65 70 75 80  
 Met Arg Tyr Pro Lys Gly Tyr Tyr Gly Gly Asn Asn Met Ile Thr Tyr  
 85 90 95  
 Gly Val Gly Val Asp Ala Val Trp Asn Phe Phe Gln Gly Ser Phe Tyr  
 100 105 110  
 Gln Asp Asp Ile Ser Val Asp Ile Gly Val Phe Gly Gly Ile Ala Ile  
 115 120 125  
 Ala Gly Asn Ser Trp Tyr Ile Gly Ser Lys Gly Gln Glu Leu Leu Gly  
 130 135 140  
 Ile Thr Asn Ser Ser Ala Val Asp Asn Thr Ser Phe Gln Phe Leu Phe  
 145 150 155 160  
 Asn Phe Gly Leu Lys Ala Leu Phe Val Asp Glu His Glu Phe Glu Ile  
 165 170 175  
 Gly Phe Lys Phe Pro Thr Ile Asn Asn Lys Tyr Tyr Thr Thr Asp Ala  
 180 185 190  
 Leu Lys Val Gln Met Arg Arg Val Phe Ala Phe Tyr Val Gly Tyr Asn  
 195 200 205  
 Tyr His Phe  
 210

<210> 309  
 <211> 517  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (51)...(464)

<400> 309  
 agatttcatt cgaggtagaa aatacattga aaaagcgtgt gaattaaacg atg gta 56  
 Met Val  
 1  
 ggg ggt gga acg gta aaa aaa gac ttg aag aaa gcc att caa tac tat 104  
 Gly Gly Gly Thr Val Lys Lys Asp Leu Lys Lys Ala Ile Gln Tyr Tyr  
 5 10 15  
 gtt aaa gcg tgt gaa ttg aat gaa atg ttt ggg tgt ctg tca tta gtt 152  
 Val Lys Ala Cys Glu Leu Asn Glu Met Phe Gly Cys Leu Ser Leu Val  
 20 25 30  
 tcg aac tct caa ata aac aaa caa aaa ctc ttt caa tat ctc tct aaa 200  
 Ser Asn Ser Gln Ile Asn Lys Gln Lys Leu Phe Gln Tyr Leu Ser Lys



<221> CDS  
<222> (51)...(398)

<400> 311  
gtggaacgct ctgtcttagc aaattgatct tagcggcgctc gtttttgata gtg gat 56  
Val Asp  
1

tca gag ggg ttt tcg cct tct att tat acc gac aag aca ggg cat ccc 104  
Ser Glu Gly Phe Ser Pro Ser Ile Tyr Thr Asp Lys Thr Gly His Pro  
5 10 15

acg att ggc tat ggc tat aat ttg agc gtt tat tct tat gag ggt aag 152  
Thr Ile Gly Tyr Gly Tyr Asn Leu Ser Val Tyr Ser Tyr Glu Gly Lys  
20 25 30

cgt atc acc aaa aca tat ggg ctt tta act gac ata ctc tct tat ggg 200  
Arg Ile Thr Lys Thr Tyr Gly Leu Leu Thr Asp Ile Leu Ser Tyr Gly  
35 40 45 50

tgg tat aaa aat ttg gac gca atg agg aga atg gtc atc ttg gat ttg 248  
Trp Tyr Lys Asn Leu Asp Ala Met Arg Arg Met Val Ile Leu Asp Leu  
55 60 65

agc tac aat tta ggc ttg aac gga ctg ctc aaa ttc aag caa ttc atc 296  
Ser Tyr Asn Leu Gly Leu Asn Gly Leu Leu Lys Phe Lys Gln Phe Ile  
70 75 80

aag gcc ata gag gat aaa aat tat gct ttg gct gtg gag aga ctg caa 344  
Lys Ala Ile Glu Asp Lys Asn Tyr Ala Leu Ala Val Glu Arg Leu Gln  
85 90 95

aaa agc ccg tat ttc aat caa gtg aaa aaa gag cgt caa gga ata tgg 392  
Lys Ser Pro Tyr Phe Asn Gln Val Lys Lys Glu Arg Gln Gly Ile Trp  
100 105 110

aaa ttt tgaaattgga gggttgcgaa aaacattgta agaaaaaata cgcaatagaa 448  
Lys Phe  
115

aag 451

<210> 312  
<211> 116  
<212> PRT  
<213> Helicobacter pylori

<400> 312  
Val Asp Ser Glu Gly Phe Ser Pro Ser Ile Tyr Thr Asp Lys Thr Gly  
1 5 10 15  
His Pro Thr Ile Gly Tyr Gly Tyr Asn Leu Ser Val Tyr Ser Tyr Glu  
20 25 30  
Gly Lys Arg Ile Thr Lys Thr Tyr Gly Leu Leu Thr Asp Ile Leu Ser  
35 40 45  
Tyr Gly Trp Tyr Lys Asn Leu Asp Ala Met Arg Arg Met Val Ile Leu  
50 55 60  
Asp Leu Ser Tyr Asn Leu Gly Leu Asn Gly Leu Leu Lys Phe Lys Gln  
65 70 75 80  
Phe Ile Lys Ala Ile Glu Asp Lys Asn Tyr Ala Leu Ala Val Glu Arg

0905913 062901

Leu	Gln	Lys	Ser	85	Pro	Tyr	Phe	Asn	Gln	90	Val	Lys	Lys	Glu	95	Arg	Gln	Gly
			100						105							110		
Ile	Trp	Lys	Phe															
			115															

<210> 313  
 <211> 399  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (50)...(346)

<400> 313  
 acacaacccat agcgacacaaa aacccgacag acccgccaag gagcgataa aac cca caa 58  
 Asn Pro Gln  
 1

agc ttt ttc agg aat acg cca cat ttt ttg atc agc cga att ttt atc 106  
 Ser Phe Phe Arg Asn Thr Pro His Phe Leu Ile Ser Arg Ile Phe Ile  
 5 10 15

cac cag cat gag aat aaa aat cag aat att gac tat gag caa cca aac 154  
 His Gln His Glu Asn Lys Asn Gln Asn Ile Asp Tyr Glu Gln Pro Asn  
 20 25 30 35

gat aga agc aaa ttc cac gct cac cct ttc aag agc gtt tta aca acc 202  
 Asp Arg Ser Lys Phe His Ala His Pro Phe Lys Ser Val Leu Thr Thr  
 40 45 50

caa acg cta cca ctt ggt ttt tta gag aga gaa aga gag aga aag caa 250  
 Gln Thr Leu Pro Leu Gly Phe Leu Glu Arg Glu Arg Glu Arg Lys Gln  
 55 60 65

aat ttt aag att gat tct caa atc tat tcc ttt gca aaa gtt aag att 298  
 Asn Phe Lys Ile Asp Ser Gln Ile Tyr Ser Phe Ala Lys Val Lys Ile  
 70 75 80

ggg tgt ttt aac atg att ttt ggc ctg ctc gca tca agc cct tat ttt 346  
 Gly Cys Phe Asn Met Ile Phe Gly Leu Leu Ala Ser Ser Pro Tyr Phe  
 85 90 95

taacatttcc gctcccttgc ttttttaaag cctccctaaa ttactacacc act 399

<210> 314  
 <211> 99  
 <212> PRT  
 <213> Helicobacter pylori

<400> 314  
 Asn Pro Gln Ser Phe Phe Arg Asn Thr Pro His Phe Leu Ile Ser Arg  
 1 5 10 15  
 Ile Phe Ile His Gln His Glu Asn Lys Asn Gln Asn Ile Asp Tyr Glu  
 20 25 30  
 Gln Pro Asn Asp Arg Ser Lys Phe His Ala His Pro Phe Lys Ser Val  
 35 40 45  
 Leu Thr Thr Gln Thr Leu Pro Leu Gly Phe Leu Glu Arg Glu Arg Glu



<210> 316  
 <211> 140  
 <212> PRT  
 <213> Helicobacter pylori

<400> 316  
 Met Ser Tyr Phe Phe Lys Ile Ile Leu Gly Thr Ser Val Ile Val Gly  
 1 5 10 15  
 Val Leu Leu Gly Leu Trp Arg Leu Thr Tyr Asp Lys Phe Tyr Phe Ser  
 20 25 30  
 Leu Val Phe Val Leu Leu Ile Leu Gly Ile Val Ala Cys Ser Tyr Ile  
 35 40 45  
 Ser Leu Lys Met His Gln Arg Lys Cys Phe Ala Lys Cys Phe Val Asn  
 50 55 60  
 Ser Glu Ser Phe Leu Ser Lys Met Leu His Ser Pro Ile Met Val Ile  
 65 70 75 80  
 Cys Phe Tyr Phe Ile Phe Ser Ile Phe Thr Ser Ile Ser Ile Val Tyr  
 85 90 95  
 Ser Val Leu Asp Tyr Asp Gln Met Met Trp Gly Phe Val Phe Cys Thr  
 100 105 110  
 Ile Val Val Cys Ala Val Val Phe Gly Thr Leu Glu Lys Asn Ala Gln  
 115 120 125  
 Glu Tyr His Gln Arg Arg Leu Phe Asp Ala Asp Val  
 130 135 140

<210> 317  
 <211> 976  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (51)...(923)

<400> 317  
 cccactgaag cgtattctaa caccctttta gaattagcta aaaaagatga aaa aat 56  
 Lys Asn  
 1  
 cgt agg cgt aac cgc ggc gat gct agc ggc aca gga tta gac aaa ctc 104  
 Arg Arg Arg Asn Arg Gly Asp Ala Ser Gly Thr Gly Leu Asp Lys Leu  
 5 10 15  
 att gac gct tan cct ttg cgc ttt ttt gat gtc gct atc gct gag caa 152  
 Ile Asp Ala Xaa Pro Leu Arg Phe Phe Asp Val Ala Ile Ala Glu Gln  
 20 25 30  
 cac gct tta act tct agc agc gct atg gct aaa gag ggg ttt aaa cct 200  
 His Ala Leu Thr Ser Ser Ser Ala Met Ala Lys Glu Gly Phe Lys Pro  
 35 40 45 50  
 ttt gtg agc atc tat tct act ttt ttg cag agg gct tat gat tct att 248  
 Phe Val Ser Ile Tyr Ser Thr Phe Leu Gln Arg Ala Tyr Asp Ser Ile  
 55 60 65  
 gtg cat gac gct tgt att tct agc ttg ccg att aaa tta gcc att gac 296  
 Val His Asp Ala Cys Ile Ser Ser Leu Pro Ile Lys Leu Ala Ile Asp  
 70 75 80

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agg gct ggg att gtg ggc gaa gat ggc gag acg cac caa ggg ctt tta	344
Arg Ala Gly Ile Val Gly Glu Asp Gly Glu Thr His Gln Gly Leu Leu	
85 90 95	
gac gtg tcg tat ttg cgc tct atc cct aac atg gtc att ttt gcc cca	392
Asp Val Ser Tyr Leu Arg Ser Ile Pro Asn Met Val Ile Phe Ala Pro	
100 105 110	
cga gac aat gag act tta aaa aac gcc gtg cgt ttt gcc aat gaa cac	440
Arg Asp Asn Glu Thr Leu Lys Asn Ala Val Arg Phe Ala Asn Glu His	
115 120 125 130	
gat tca agc cct tgc gcg ttc cga tac cct agg ggg tcg ttt gcg tta	488
Asp Ser Ser Pro Cys Ala Phe Arg Tyr Pro Arg Gly Ser Phe Ala Leu	
135 140 145	
aaa gag ggg gtt ttt gag cct agc ggt ttt gtt tta ggc caa agc gaa	536
Lys Glu Gly Val Phe Glu Pro Ser Gly Phe Val Leu Gly Gln Ser Glu	
150 155 160	
ttg ttg aaa aaa gag ggc gaa att tta ctc ata ggc tat ggt aat ggc	584
Leu Leu Lys Lys Glu Gly Glu Ile Leu Leu Ile Gly Tyr Gly Asn Gly	
165 170 175	
gtg ggg cgg gcg cat tta gtc caa ctg gct tta aaa gaa aaa aac ata	632
Val Gly Arg Ala His Leu Val Gln Leu Ala Leu Lys Glu Lys Asn Ile	
180 185 190	
gaa tgc gct ctc ttg gat ctc agg ttt tta aag cct tta gat cca aat	680
Glu Cys Ala Leu Leu Asp Leu Arg Phe Leu Lys Pro Leu Asp Pro Asn	
195 200 205 210	
tta agc gcg atc gtt gcc cct tat caa aag ctc tat gtt ttt agc gat	728
Leu Ser Ala Ile Val Ala Pro Tyr Gln Lys Leu Tyr Val Phe Ser Asp	
215 220 225	
aat tac aag ctt gga ggg gtg gct agc gcg att tta gag ttt ttg agc	776
Asn Tyr Lys Leu Gly Gly Val Ala Ser Ala Ile Leu Glu Phe Leu Ser	
230 235 240	
gaa caa aat att tta aag cct gtt aaa agc ttt gaa atc att gat gaa	824
Glu Gln Asn Ile Leu Lys Pro Val Lys Ser Phe Glu Ile Ile Asp Glu	
245 250 255	
ttt atc atg cat ggg aac acc gct tta gtg gaa aaa tcc tta gga tta	872
Phe Ile Met His Gly Asn Thr Ala Leu Val Glu Lys Ser Leu Gly Leu	
260 265 270	
gac aca gag agt ttg act gac gct att tta aaa gat tta gga caa gag	920
Asp Thr Glu Ser Leu Thr Asp Ala Ile Leu Lys Asp Leu Gly Gln Glu	
275 280 285 290	
aga tgaaaaacaaa agcgccaatg aaaaatatcc gcaatttttc cattatcgct	973
cac	976

<210> 318  
 <211> 291  
 <212> PRT  
 <213> Helicobacter pylori

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<400> 318
Lys Asn Arg Arg Arg Asn Arg Gly Asp Ala Ser Gly Thr Gly Leu Asp
 1          5          10          15
Lys Leu Ile Asp Ala Xaa Pro Leu Arg Phe Phe Asp Val Ala Ile Ala
 20          25          30
Glu Gln His Ala Leu Thr Ser Ser Ala Met Ala Lys Glu Gly Phe
 35          40          45
Lys Pro Phe Val Ser Ile Tyr Ser Thr Phe Leu Gln Arg Ala Tyr Asp
 50          55          60
Ser Ile Val His Asp Ala Cys Ile Ser Ser Leu Pro Ile Lys Leu Ala
 65          70          75          80
Ile Asp Arg Ala Gly Ile Val Gly Glu Asp Gly Glu Thr His Gln Gly
 85          90          95
Leu Leu Asp Val Ser Tyr Leu Arg Ser Ile Pro Asn Met Val Ile Phe
100          105          110
Ala Pro Arg Asp Asn Glu Thr Leu Lys Asn Ala Val Arg Phe Ala Asn
115          120          125
Glu His Asp Ser Ser Pro Cys Ala Phe Arg Tyr Pro Arg Gly Ser Phe
130          135          140
Ala Leu Lys Glu Gly Val Phe Glu Pro Ser Gly Phe Val Leu Gly Gln
145          150          155          160
Ser Glu Leu Leu Lys Lys Glu Gly Glu Ile Leu Leu Ile Gly Tyr Gly
165          170          175
Asn Gly Val Gly Arg Ala His Leu Val Gln Leu Ala Leu Lys Glu Lys
180          185          190
Asn Ile Glu Cys Ala Leu Leu Asp Leu Arg Phe Leu Lys Pro Leu Asp
195          200          205
Pro Asn Leu Ser Ala Ile Val Ala Pro Tyr Gln Lys Leu Tyr Val Phe
210          215          220
Ser Asp Asn Tyr Lys Leu Gly Gly Val Ala Ser Ala Ile Leu Glu Phe
225          230          235          240
Leu Ser Glu Gln Asn Ile Leu Lys Pro Val Lys Ser Phe Glu Ile Ile
245          250          255
Asp Glu Phe Ile Met His Gly Asn Thr Ala Leu Val Glu Lys Ser Leu
260          265          270
Gly Leu Asp Thr Glu Ser Leu Thr Asp Ala Ile Leu Lys Asp Leu Gly
275          280          285
Gln Glu Arg
290

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<210> 319
<211> 1135
<212> DNA
<213> Helicobacter pylori

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<220>
<221> CDS
<222> (51)...(1082)

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<400> 319
ggattaagat gttataatag ttgttat tttt ttcatttttaa aaggggtttt atg gca      56
                                     Met Ala
                                     1

tta tta ttc aca gga gcg tgc ggg tat ata ggc tcg cat acc gca agg      104
Leu Leu Phe Thr Gly Ala Cys Gly Tyr Ile Gly Ser His Thr Ala Arg
 5          10          15

gcg ttt tta gaa aaa acc aaa gaa aat atc att att gta gat gac tta      152

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Ala	Phe	Leu	Glu	Lys	Thr	Lys	Glu	Asn	Ile	Ile	Ile	Val	Asp	Asp	Leu		
	20					25					30						
agc	acc	ggg	ttt	tta	gag	cac	ctc	aaa	gcg	tta	gag	cat	tat	tac	cct	200	
Ser	Thr	Gly	Phe	Leu	Glu	His	Leu	Lys	Ala	Leu	Glu	His	Tyr	Tyr	Pro		
	35				40					45					50		
aat	agg	gtt	gtg	ttt	att	caa	gcg	aat	ttg	aat	gaa	acg	cac	aaa	tta	248	
Asn	Arg	Val	Val	Phe	Ile	Gln	Ala	Asn	Leu	Asn	Glu	Thr	His	Lys	Leu		
				55					60					65			
gac	gcc	ttt	ttg	aat	aag	cag	cag	cta	aaa	gat	ccc	att	gaa	gcc	atc	296	
Asp	Ala	Phe	Leu	Asn	Lys	Gln	Gln	Leu	Lys	Asp	Pro	Ile	Glu	Ala	Ile		
			70					75					80				
ttg	cac	ttt	ggg	gct	aaa	atc	tca	gta	gaa	gaa	tcc	acg	cac	ttg	cct	344	
Leu	His	Phe	Gly	Ala	Lys	Ile	Ser	Val	Glu	Glu	Ser	Thr	His	Leu	Pro		
		85					90					95					
tta	gaa	tac	tac	acc	aac	aac	acg	ctc	aac	act	tta	gag	ctt	gtc	aaa	392	
Leu	Glu	Tyr	Tyr	Thr	Asn	Asn	Thr	Leu	Asn	Thr	Leu	Glu	Leu	Val	Lys		
	100					105					110						
ctt	tgc	tta	aaa	cat	gca	atc	aag	cgt	ttt	att	ttt	tct	tct	acg	gcc	440	
Leu	Cys	Leu	Lys	His	Ala	Ile	Lys	Arg	Phe	Ile	Phe	Ser	Ser	Thr	Ala		
	115				120				125						130		
gtg	gtt	tat	ggc	gaa	tct	agt	tca	agt	ttg	aat	gaa	gaa	agc	ccc	tta	488	
Val	Val	Tyr	Gly	Glu	Ser	Ser	Ser	Ser	Leu	Asn	Glu	Glu	Ser	Pro	Leu		
			135						140					145			
aac	ccc	att	aat	cct	tat	gga	gcg	tct	aaa	atg	atg	agc	gaa	aga	atc	536	
Asn	Pro	Ile	Asn	Pro	Tyr	Gly	Ala	Ser	Lys	Met	Met	Ser	Glu	Arg	Ile		
			150					155					160				
ttg	tta	gac	act	tct	aaa	ata	gcg	gat	ttt	aaa	tgc	gtt	att	ttg	cgc	584	
Leu	Leu	Asp	Thr	Ser	Lys	Ile	Ala	Asp	Phe	Lys	Cys	Val	Ile	Leu	Arg		
		165					170					175					
tat	ttc	aat	gtg	gct	ggg	gca	tgc	atg	cac	aat	gat	tat	acc	acc	cct	632	
Tyr	Phe	Asn	Val	Ala	Gly	Ala	Cys	Met	His	Asn	Asp	Tyr	Thr	Thr	Pro		
	180					185					190						
tac	acg	cta	ggg	caa	cgc	acg	ctc	aac	gcc	acg	cat	ttg	atc	aaa	atc	680	
Tyr	Thr	Leu	Gly	Gln	Arg	Thr	Leu	Asn	Ala	Thr	His	Leu	Ile	Lys	Ile		
	195				200				205					210			
gca	tgc	gaa	tgc	gcg	gtg	ggg	aaa	agg	aaa	aaa	atg	ggg	att	ttt	ggc	728	
Ala	Cys	Glu	Cys	Ala	Val	Gly	Lys	Arg	Lys	Lys	Met	Gly	Ile	Phe	Gly		
				215					220					225			
act	aac	tac	ccc	aca	aga	gat	ggc	act	tgc	att	agg	gat	tat	atc	cat	776	
Thr	Asn	Tyr	Pro	Thr	Arg	Asp	Gly	Thr	Cys	Ile	Arg	Asp	Tyr	Ile	His		
			230				235						240				
gta	gat	gat	ttg	gct	aac	gca	cat	tta	gcg	agc	tat	caa	acc	ctt	tta	824	
Val	Asp	Asp	Leu	Ala	Asn	Ala	His	Leu	Ala	Ser	Tyr	Gln	Thr	Leu	Leu		
		245					250					255					

gaa aaa aat aag agc gag atc tat aat gtc ggc tac aat caa ggc cat 872  
 Glu Lys Asn Lys Ser Glu Ile Tyr Asn Val Gly Tyr Asn Gln Gly His  
 260 265 270

agc gtg aaa gaa gtg ata gaa aag gtc aaa gaa atc tca aac aac gat 920  
 Ser Val Lys Glu Val Ile Glu Lys Val Lys Glu Ile Ser Asn Asn Asp  
 275 280 285 290

ttt tta gtg gaa att tta gac aaa cga cag ggc gat cca gca agc ctt 968  
 Phe Leu Val Glu Ile Leu Asp Lys Arg Gln Gly Asp Pro Ala Ser Leu  
 295 300 305

att gcc aat aac gct aaa atc tta caa aac acc tct ttc aaa ccc ctt 1016  
 Ile Ala Asn Asn Ala Lys Ile Leu Gln Asn Thr Ser Phe Lys Pro Leu  
 310 315 320

tat aac aac cta gac acc att atc aaa agc gct cta gat tgg gaa gaa 1064  
 Tyr Asn Asn Leu Asp Thr Ile Ile Lys Ser Ala Leu Asp Trp Glu Glu  
 325 330 335

cac ctt ttg agg ttt caa taatacaccc tgtgcaaata caagccatta 1112  
 His Leu Leu Arg Phe Gln  
 340

gccattatgg gcgttcttat agt 1135

<210> 320  
 <211> 344  
 <212> PRT  
 <213> Helicobacter pylori

<400> 320  
 Met Ala Leu Leu Phe Thr Gly Ala Cys Gly Tyr Ile Gly Ser His Thr  
 1 5 10 15  
 Ala Arg Ala Phe Leu Glu Lys Thr Lys Glu Asn Ile Ile Ile Val Asp  
 20 25 30  
 Asp Leu Ser Thr Gly Phe Leu Glu His Leu Lys Ala Leu Glu His Tyr  
 35 40 45  
 Tyr Pro Asn Arg Val Val Phe Ile Gln Ala Asn Leu Asn Glu Thr His  
 50 55 60  
 Lys Leu Asp Ala Phe Leu Asn Lys Gln Gln Leu Lys Asp Pro Ile Glu  
 65 70 75 80  
 Ala Ile Leu His Phe Gly Ala Lys Ile Ser Val Glu Glu Ser Thr His  
 85 90 95  
 Leu Pro Leu Glu Tyr Tyr Thr Asn Asn Thr Leu Asn Thr Leu Glu Leu  
 100 105 110  
 Val Lys Leu Cys Leu Lys His Ala Ile Lys Arg Phe Ile Phe Ser Ser  
 115 120 125  
 Thr Ala Val Val Tyr Gly Glu Ser Ser Ser Ser Leu Asn Glu Glu Ser  
 130 135 140  
 Pro Leu Asn Pro Ile Asn Pro Tyr Gly Ala Ser Lys Met Met Ser Glu  
 145 150 155 160  
 Arg Ile Leu Leu Asp Thr Ser Lys Ile Ala Asp Phe Lys Cys Val Ile  
 165 170 175  
 Leu Arg Tyr Phe Asn Val Ala Gly Ala Cys Met His Asn Asp Tyr Thr  
 180 185 190  
 Thr Pro Tyr Thr Leu Gly Gln Arg Thr Leu Asn Ala Thr His Leu Ile  
 195 200 205  
 Lys Ile Ala Cys Glu Cys Ala Val Gly Lys Arg Lys Lys Met Gly Ile

210		215		220
Phe Gly Thr Asn Tyr	Pro Thr Arg Asp Gly Thr Cys Ile Arg Asp Tyr			
225	230	235	240	
Ile His Val Asp	Leu Ala Asn Ala His Leu Ala Ser Tyr Gln Thr			
	245	250	255	
Leu Leu Glu Lys Asn Lys Ser Glu Ile Tyr Asn Val Gly Tyr Asn Gln				
	260	265	270	
Gly His Ser Val Lys Glu Val Ile Glu Lys Val Lys Glu Ile Ser Asn				
	275	280	285	
Asn Asp Phe Leu Val Glu Ile Leu Asp Lys Arg Gln Gly Asp Pro Ala				
	290	295	300	
Ser Leu Ile Ala Asn Asn Ala Lys Ile Leu Gln Asn Thr Ser Phe Lys				
305	310	315	320	
Pro Leu Tyr Asn Asn Leu Asp Thr Ile Ile Lys Ser Ala Leu Asp Trp				
	325	330	335	
Glu Glu His Leu Leu Arg Phe Gln				
	340			

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 <211> 1170  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (97)...(1119)

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atcattgaga tagttttaag gaaattaagg aacaaa atg gaa gtt tca cgc aag	114
	Met Glu Val Ser Arg Lys
	1 5
aaa att tac aac ccc aat tct aca gaa agt gtg aat gaa aga aag att	162
Lys Ile Tyr Asn Pro Asn Ser Thr Glu Ser Val Asn Glu Arg Lys Ile	
	10 15 20
ttt ggg ggc aat cct aca agc atg ttt gat ttg aat aag atc aag tat	210
Phe Gly Gly Asn Pro Thr Ser Met Phe Asp Leu Asn Lys Ile Lys Tyr	
	25 30 35
caa tgg gcg gat cat ttg tgg aaa acg atg ctc gct aac acc tgg ttt	258
Gln Trp Ala Asp His Leu Trp Lys Thr Met Leu Ala Asn Thr Trp Phe	
	40 45 50
gct gaa gaa gtg agc atg aat gat gac aaa agg gat tat ttg aaa tta	306
Ala Glu Glu Val Ser Met Asn Asp Asp Lys Arg Asp Tyr Leu Lys Leu	
	55 60 65 70
agc gca gag gaa aag atc ggt tat gac aga gct tta gcg caa ctc att	354
Ser Ala Glu Glu Lys Ile Gly Tyr Asp Arg Ala Leu Ala Gln Leu Ile	
	75 80 85
ttt atg gac agc ttg caa gcg aat aat tta att gac aat atc aat ccc	402
Phe Met Asp Ser Leu Gln Ala Asn Asn Leu Ile Asp Asn Ile Asn Pro	
	90 95 100
ttc atc acc agc ccc gaa atc aat ttg tgt ttg gtg cgt caa gct tat	450
Phe Ile Thr Ser Pro Glu Ile Asn Leu Cys Leu Val Arg Gln Ala Tyr	

006290.062901

105	110	115	
gaa gaa gcc cta cac agc cat gcg tat gcg gtg atg gta gaa agc ata Glu Glu Ala Leu His Ser His Ala Tyr Ala Val Met Val Glu Ser Ile 120 125 130			498
agt gcg aat act gaa gag att tat gac atg tgg cgt aac gat atg caa Ser Ala Asn Thr Glu Glu Ile Tyr Asp Met Trp Arg Asn Asp Met Gln 135 140 145 150			546
tta aaa agc aag aac gac tat atc gcg caa gtg tat atg gaa tta gcc Leu Lys Ser Lys Asn Asp Tyr Ile Ala Gln Val Tyr Met Glu Leu Ala 155 160 165			594
aaa aac ccc aca gaa gaa aac att ctc aaa gcg ctt ttt gct aac cag Lys Asn Pro Thr Glu Glu Asn Ile Leu Lys Ala Leu Phe Ala Asn Gln 170 175 180			642
att tta gag ggg att tat ttt tat agc ggg ttt agc tat ttt tac act Ile Leu Glu Gly Ile Tyr Phe Tyr Ser Gly Phe Ser Tyr Phe Tyr Thr 185 190 195			690
ttg gct agg agc ggt aaa atg cta gga tgc gca caa atg att cgt ttt Leu Ala Arg Ser Gly Lys Met Leu Gly Ser Ala Gln Met Ile Arg Phe 200 205 210			738
atc caa aga gat gag gta acg cat ttg att ttg ttc caa aac atg atc Ile Gln Arg Asp Glu Val Thr His Leu Ile Leu Phe Gln Asn Met Ile 215 220 225 230			786
aac gct tta agg aat gaa aga gcg gat ctc ttc acg ccg caa ttg att Asn Ala Leu Arg Asn Glu Arg Ala Asp Leu Phe Thr Pro Gln Leu Ile 235 240 245			834
aat gaa gtc ata gga atg ttt aaa aaa gcg gta gaa att gaa gct ttg Asn Glu Val Ile Gly Met Phe Lys Lys Ala Val Glu Ile Glu Ala Leu 250 255 260			882
tgg ggg gat tat atc acg caa ggc aag att tta ggg ctc act tca agc Trp Gly Asp Tyr Ile Thr Gln Gly Lys Ile Leu Gly Leu Thr Ser Ser 265 270 275			930
ttg att gag caa tac atc cag ttt tta gcg gat agc cgt ttg agt aag Leu Ile Glu Gln Tyr Ile Gln Phe Leu Ala Asp Ser Arg Leu Ser Lys 280 285 290			978
gtg ggc atc gct aaa gtt tat ggc gtc caa cac ccc att aaa tgg gta Val Gly Ile Ala Lys Val Tyr Gly Val Gln His Pro Ile Lys Trp Val 295 300 305 310			1026
gag agc ttt tca agt ttc aat gag cag cgc tct aat ttc ttt gag gct Glu Ser Phe Ser Ser Phe Asn Glu Gln Arg Ser Asn Phe Phe Glu Ala 315 320 325			1074
agg gtg agc aat tac gct aaa ggg agc gtg agt ttt gat gat ttt Arg Val Ser Asn Tyr Ala Lys Gly Ser Val Ser Phe Asp Asp Phe 330 335 340			1119
taaggggctt gtttgaatag tattaaaaac catttaatgt gtgaagaaat c			1170

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 <211> 341  
 <212> PRT  
 <213> Helicobacter pylori

<400> 322  
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 1 5 10 15  
 Val Asn Glu Arg Lys Ile Phe Gly Gly Asn Pro Thr Ser Met Phe Asp  
 20 25 30  
 Leu Asn Lys Ile Lys Tyr Gln Trp Ala Asp His Leu Trp Lys Thr Met  
 35 40 45  
 Leu Ala Asn Thr Trp Phe Ala Glu Glu Val Ser Met Asn Asp Asp Lys  
 50 55 60  
 Arg Asp Tyr Leu Lys Leu Ser Ala Glu Glu Lys Ile Gly Tyr Asp Arg  
 65 70 75 80  
 Ala Leu Ala Gln Leu Ile Phe Met Asp Ser Leu Gln Ala Asn Asn Leu  
 85 90 95  
 Ile Asp Asn Ile Asn Pro Phe Ile Thr Ser Pro Glu Ile Asn Leu Cys  
 100 105 110  
 Leu Val Arg Gln Ala Tyr Glu Glu Ala Leu His Ser His Ala Tyr Ala  
 115 120 125  
 Val Met Val Glu Ser Ile Ser Ala Asn Thr Glu Glu Ile Tyr Asp Met  
 130 135 140  
 Trp Arg Asn Asp Met Gln Leu Lys Ser Lys Asn Asp Tyr Ile Ala Gln  
 145 150 155 160  
 Val Tyr Met Glu Leu Ala Lys Asn Pro Thr Glu Glu Asn Ile Leu Lys  
 165 170 175  
 Ala Leu Phe Ala Asn Gln Ile Leu Glu Gly Ile Tyr Phe Tyr Ser Gly  
 180 185 190  
 Phe Ser Tyr Phe Tyr Thr Leu Ala Arg Ser Gly Lys Met Leu Gly Ser  
 195 200 205  
 Ala Gln Met Ile Arg Phe Ile Gln Arg Asp Glu Val Thr His Leu Ile  
 210 215 220  
 Leu Phe Gln Asn Met Ile Asn Ala Leu Arg Asn Glu Arg Ala Asp Leu  
 225 230 235 240  
 Phe Thr Pro Gln Leu Ile Asn Glu Val Ile Gly Met Phe Lys Lys Ala  
 245 250 255  
 Val Glu Ile Glu Ala Leu Trp Gly Asp Tyr Ile Thr Gln Gly Lys Ile  
 260 265 270  
 Leu Gly Leu Thr Ser Ser Leu Ile Glu Gln Tyr Ile Gln Phe Leu Ala  
 275 280 285  
 Asp Ser Arg Leu Ser Lys Val Gly Ile Ala Lys Val Tyr Gly Val Gln  
 290 295 300  
 His Pro Ile Lys Trp Val Glu Ser Phe Ser Ser Phe Asn Glu Gln Arg  
 305 310 315 320  
 Ser Asn Phe Phe Glu Ala Arg Val Ser Asn Tyr Ala Lys Gly Ser Val  
 325 330 335  
 Ser Phe Asp Asp Phe  
 340

<210> 323  
 <211> 689  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
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 <222> (139)...(627)

09591.065860

0989513.062901 ET 1556860

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 tttttgttg attctaac atg aaa gat ttt tat ttc atg gag atg aac act 171  
 Met Lys Asp Phe Tyr Phe Met Glu Met Asn Thr  
 1 5 10

cgt ttg caa gtg gaa cac acc att agc gaa atg gtg agc ggg tta aac 219  
 Arg Leu Gln Val Glu His Thr Ile Ser Glu Met Val Ser Gly Leu Asn  
 15 20 25

ctc att gag tgg atg att aaa atc gct caa ggc gaa aaa ttg ccc aag 267  
 Leu Ile Glu Trp Met Ile Lys Ile Ala Gln Gly Glu Lys Leu Pro Lys  
 30 35 40

caa gaa agc ttt tct ctc aaa ggc cat gcg ata gaa tgc cga atc acg 315  
 Gln Glu Ser Phe Ser Leu Lys Gly His Ala Ile Glu Cys Arg Ile Thr  
 45 50 55

gca gaa gat cct aaa aaa ttc tac cca agc ccg ggc aaa att acc gaa 363  
 Ala Glu Asp Pro Lys Lys Phe Tyr Pro Ser Pro Gly Lys Ile Thr Glu  
 60 65 70 75

tgg atc gct cct ggt ggg gtg aat gtg cgc ctt gat tcg cac gcg cat 411  
 Trp Ile Ala Pro Gly Gly Val Asn Val Arg Leu Asp Ser His Ala His  
 80 85 90

gcc aat tat gtc gtg cct acg cac tat gat tcg atg att ggc aag ctc 459  
 Ala Asn Tyr Val Val Pro Thr His Tyr Asp Ser Met Ile Gly Lys Leu  
 95 100 105

att gtg tgg ggt gaa aac aga gaa aga gcg atc gct aag atg aaa agg 507  
 Ile Val Trp Gly Glu Asn Arg Glu Arg Ala Ile Ala Lys Met Lys Arg  
 110 115 120

gct tta aag gaa ttt aaa gta gaa ggc att aaa acg acc att cct ttc 555  
 Ala Leu Lys Glu Phe Lys Val Glu Gly Ile Lys Thr Thr Ile Pro Phe  
 125 130 135

cac ctt gaa atg ctt gaa aat gcg gat ttc agg caa gca aaa atc cac 603  
 His Leu Glu Met Leu Glu Asn Ala Asp Phe Arg Gln Ala Lys Ile His  
 140 145 150 155

acg aag tat tta gaa gaa aat ttt taagttttta ggattctttt aagcatagtt 657  
 Thr Lys Tyr Leu Glu Glu Asn Phe  
 160

taagggtttt aagcgatcag aaaaagtcag ca 689

<210> 324  
 <211> 163  
 <212> PRT  
 <213> Helicobacter pylori

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 Met Lys Asp Phe Tyr Phe Met Glu Met Asn Thr Arg Leu Gln Val Glu  
 1 5 10 15  
 His Thr Ile Ser Glu Met Val Ser Gly Leu Asn Leu Ile Glu Trp Met  
 20 25 30



Ile Lys Ile Ala Gln Gly Glu Lys Leu Pro Lys Gln Glu Ser Phe Ser  
 35 40 45  
 Leu Lys Gly His Ala Ile Glu Cys Arg Ile Thr Ala Glu Asp Pro Lys  
 50 55 60  
 Lys Phe Tyr Pro Ser Pro Gly Lys Ile Thr Glu Trp Ile Ala Pro Gly  
 65 70 75 80  
 Gly Val Asn Val Arg Leu Asp Ser His Ala His Ala Asn Tyr Val Val  
 85 90 95  
 Pro Thr His Tyr Asp Ser Met Ile Gly Lys Leu Ile Val Trp Gly Glu  
 100 105 110  
 Asn Arg Glu Arg Ala Ile Ala Lys Met Lys Arg Ala Leu Lys Glu Phe  
 115 120 125  
 Lys Val Glu Gly Ile Lys Thr Thr Ile Pro Phe His Leu Glu Met Leu  
 130 135 140  
 Glu Asn Ala Asp Phe Arg Gln Ala Lys Ile His Thr Lys Tyr Leu Glu  
 145 150 155 160  
 Glu Asn Phe

<210> 325  
 <211> 1960  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (51)...(1907)

<400> 325  
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 Met Phe  
 1  
 tat cac tta atc gct cct tta aaa aat aaa acc ccc cct tta acc tat 104  
 Tyr His Leu Ile Ala Pro Leu Lys Asn Lys Thr Pro Pro Leu Thr Tyr  
 5 10 15  
 ttt tct aaa gag caa cac caa aaa gga gcg tta gtc aat atc cct tta 152  
 Phe Ser Lys Glu Gln His Gln Lys Gly Ala Leu Val Asn Ile Pro Leu  
 20 25 30  
 agg aat aaa acg ctt tta ggc gtc gtc ctt gaa gaa gtt tca aaa ccc 200  
 Arg Asn Lys Thr Leu Leu Gly Val Val Leu Glu Glu Val Ser Lys Pro  
 35 40 45 50  
 tct ttt gaa tgc cta gag cta gaa aaa acc cct tat ttt tta ctc ccc 248  
 Ser Phe Glu Cys Leu Glu Leu Glu Lys Thr Pro Tyr Phe Leu Leu Pro  
 55 60 65  
 ttt caa atg gag ctc gct att ttt atc gct caa tat tac tca gct aat 296  
 Phe Gln Met Glu Leu Ala Ile Phe Ile Ala Gln Tyr Tyr Ser Ala Asn  
 70 75 80  
 ctt tct tca gtt tta agc ctt ttt gcc cct ttt aaa gaa tgc gat tta 344  
 Leu Ser Ser Val Leu Ser Leu Phe Ala Pro Phe Lys Glu Cys Asp Leu  
 85 90 95  
 gtg ggg tta gaa aaa att gag cct att ctt aat ata tta agc caa acg 392  
 Val Gly Leu Glu Lys Ile Glu Pro Ile Leu Asn Ile Leu Ser Gln Thr

100	105	110	
caa aca aac gct tta aaa gaa ttg caa aaa cat tca gca agc ttg ctc Gln Thr Asn Ala Leu Lys Glu Leu Gln Lys His Ser Ala Ser Leu Leu 115 120 125 130			440
ttt ggc gat acg ggt agc ggg aaa acc gag att tat atg cat gca atc Phe Gly Asp Thr Gly Ser Gly Lys Thr Glu Ile Tyr Met His Ala Ile 135 140 145			488
gcc caa act tta gag caa aaa aaa agc gct tta ttg ttg gtg cca gaa Ala Gln Thr Leu Glu Gln Lys Lys Ser Ala Leu Leu Leu Val Pro Glu 150 155 160			536
atc gct ctc acc cct caa atg caa caa cgc ctt aaa agg gtt ttt aaa Ile Ala Leu Thr Pro Gln Met Gln Gln Arg Leu Lys Arg Val Phe Lys 165 170 175			584
gaa aat tta ggc ttg tgg cat agc aaa ctc tct caa aat caa aaa aaa Glu Asn Leu Gly Leu Trp His Ser Lys Leu Ser Gln Asn Gln Lys Lys 180 185 190			632
caa ttt tta gaa aag ctt tat tcg caa gaa atc aaa tta gtg gta ggc Gln Phe Leu Glu Lys Leu Tyr Ser Gln Glu Ile Lys Leu Val Val Gly 195 200 205 210			680
aca cga agc gcg ttg ttt tta ccc ctt aaa gag ctg ggt tta atc att Thr Arg Ser Ala Leu Phe Leu Pro Leu Lys Glu Leu Gly Leu Ile Ile 215 220 225			728
gta gat gaa gag cat gac ttt tct tat aaa tcc cat caa agc cct atg Val Asp Glu Glu His Asp Phe Ser Tyr Lys Ser His Gln Ser Pro Met 230 235 240			776
tat aac gct agg gat tta tgc ttg tat tta tct cat aaa ttc cct att Tyr Asn Ala Arg Asp Leu Cys Leu Tyr Leu Ser His Lys Phe Pro Ile 245 250 255			824
caa gtg atc tta ggc tct gct acg cca agt ttg aat agt tat aaa cgc Gln Val Ile Leu Gly Ser Ala Thr Pro Ser Leu Asn Ser Tyr Lys Arg 260 265 270			872
ttt aaa gat aag gct tta gtg cgc tta aag ggg cgc tac acc ccc acg Phe Lys Asp Lys Ala Leu Val Arg Leu Lys Gly Arg Tyr Thr Pro Thr 275 280 285 290			920
caa aaa aac att att ttt gaa aaa acc gag cgt ttt atc acg ccc aaa Gln Lys Asn Ile Ile Phe Glu Lys Thr Glu Arg Phe Ile Thr Pro Lys 295 300 305			968
ctc cta gaa gcg cta caa caa gtc cta gac aaa aac gag caa gcc att Leu Leu Glu Ala Leu Gln Gln Val Leu Asp Lys Asn Glu Gln Ala Ile 310 315 320			1016
att ttt gtg cct aca agg gct aat ttc aaa acc ttg ctg tgc caa agt Ile Phe Val Pro Thr Arg Ala Asn Phe Lys Thr Leu Leu Cys Gln Ser 325 330 335			1064
tgt tac aaa agc gtt caa tgc ccc ttt tgc agc gtg aat atg agc ttg			1112

0065913-062901 ET 55860

Cys	Tyr	Lys	Ser	Val	Gln	Cys	Pro	Phe	Cys	Ser	Val	Asn	Met	Ser	Leu	
340						345					350					
cat	tta	aag	acc	aac	aaa	ctc	atg	tgc	cat	tat	tgc	cat	ttt	tca	agc	1160
His	Leu	Lys	Thr	Asn	Lys	Leu	Met	Cys	His	Tyr	Cys	His	Phe	Ser	Ser	
355					360					365					370	
cct	atc	cct	aaa	att	tgc	agc	gcg	tgt	caa	agc	gaa	gtc	tta	gtg	ggc	1208
Pro	Ile	Pro	Lys	Ile	Cys	Ser	Ala	Cys	Gln	Ser	Glu	Val	Leu	Val	Gly	
				375					380					385		
aaa	agg	ata	ggc	act	atg	caa	gtg	cta	aag	gaa	tta	gag	agc	ctt	tta	1256
Lys	Arg	Ile	Gly	Thr	Met	Gln	Val	Leu	Lys	Glu	Leu	Glu	Ser	Leu	Leu	
			390					395					400			
gag	ggg	gct	aaa	ata	gcg	att	tta	gat	aaa	gat	cac	act	agc	acg	caa	1304
Glu	Gly	Ala	Lys	Ile	Ala	Ile	Leu	Asp	Lys	Asp	His	Thr	Ser	Thr	Gln	
		405					410					415				
aaa	aaa	ctc	cac	aat	att	tta	aac	gat	ttc	aac	gct	caa	aaa	acg	aat	1352
Lys	Lys	Leu	His	Asn	Ile	Leu	Asn	Asp	Phe	Asn	Ala	Gln	Lys	Thr	Asn	
		420				425					430					
atc	tta	atc	ggc	act	caa	atg	ata	agc	aaa	ggg	cat	gat	tac	gct	aaa	1400
Ile	Leu	Ile	Gly	Thr	Gln	Met	Ile	Ser	Lys	Gly	His	Asp	Tyr	Ala	Lys	
435					440					445					450	
gtg	agt	ttg	gcg	gtt	gtt	tta	ggc	ata	gac	aat	atc	atc	aaa	tct	aat	1448
Val	Ser	Leu	Ala	Val	Val	Leu	Gly	Ile	Asp	Asn	Ile	Ile	Lys	Ser	Asn	
				455					460					465		
agt	tat	agg	gct	tta	gaa	gaa	ggc	gtg	tcg	tta	ctt	tat	caa	atc	gct	1496
Ser	Tyr	Arg	Ala	Leu	Glu	Glu	Gly	Val	Ser	Leu	Leu	Tyr	Gln	Ile	Ala	
			470					475					480			
ggg	agg	agc	gct	agg	caa	att	tct	ggc	caa	gtg	ttc	att	caa	agc	acc	1544
Gly	Arg	Ser	Ala	Arg	Gln	Ile	Ser	Gly	Gln	Val	Phe	Ile	Gln	Ser	Thr	
			485				490					495				
gaa	acc	gat	ctg	tta	gaa	aat	ttc	tta	gaa	gat	tat	gaa	gat	ttt	tta	1592
Glu	Thr	Asp	Leu	Leu	Glu	Asn	Phe	Leu	Glu	Asp	Tyr	Glu	Asp	Phe	Leu	
			500			505					510					
caa	tac	gaa	ttg	caa	gaa	agg	tgc	gaa	ctc	tac	ccg	cct	ttt	tct	agg	1640
Gln	Tyr	Glu	Leu	Gln	Glu	Arg	Cys	Glu	Leu	Tyr	Pro	Pro	Phe	Ser	Arg	
515					520					525					530	
ctg	tgt	ttg	ttg	gag	ttt	aag	cat	aaa	aac	gaa	gaa	aaa	gcc	caa	caa	1688
Leu	Cys	Leu	Leu	Glu	Phe	Lys	His	Lys	Asn	Glu	Glu	Lys	Ala	Gln	Gln	
				535					540					545		
ttg	agc	cta	aaa	gcc	tct	caa	acc	ctt	tct	tcg	tgt	tta	gaa	aag	ggc	1736
Leu	Ser	Leu	Lys	Ala	Ser	Gln	Thr	Leu	Ser	Ser	Cys	Leu	Glu	Lys	Gly	
			550					555					560			
gta	acg	ctc	tct	aat	ttc	aaa	gcc	ccc	att	gaa	aaa	atc	gct	tct	tct	1784
Val	Thr	Leu	Ser	Asn	Phe	Lys	Ala	Pro	Ile	Glu	Lys	Ile	Ala	Ser	Ser	
			565				570					575				

tat	cgc	tac	ctt	att	tta	ttg	cgt	tcc	aaa	aac	cct	tta	agc	cta	atc	1832
Tyr	Arg	Tyr	Leu	Ile	Leu	Leu	Arg	Ser	Lys	Asn	Pro	Leu	Ser	Leu	Ile	
	580					585					590					

aaa	agc	gtg	cat	gcg	ttt	tta	aaa	tcc	gcc	cct	agt	atc	cct	tgc	agc	1880
Lys	Ser	Val	His	Ala	Phe	Leu	Lys	Ser	Ala	Pro	Ser	Ile	Pro	Cys	Ser	
	595				600					605					610	

gtg	aac	atg	gat	cct	gtg	gat	att	ttt	taaaaaactc	atgttttata	1927
Val	Asn	Met	Asp	Pro	Val	Asp	Ile	Phe			
					615						

tattattttca	aaaaacttaa	gtttttctgg	cga	1960
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 <211> 619  
 <212> PRT  
 <213> Helicobacter pylori

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Thr	Tyr	Phe	Ser	Lys	Glu	Gln	His	Gln	Lys	Gly	Ala	Leu	Val	Asn	Ile
			20					25					30		
Pro	Leu	Arg	Asn	Lys	Thr	Leu	Leu	Gly	Val	Val	Leu	Glu	Glu	Val	Ser
		35					40					45			
Lys	Pro	Ser	Phe	Glu	Cys	Leu	Glu	Leu	Glu	Lys	Thr	Pro	Tyr	Phe	Leu
	50					55					60				
Leu	Pro	Phe	Gln	Met	Glu	Leu	Ala	Ile	Phe	Ile	Ala	Gln	Tyr	Tyr	Ser
65					70					75					80
Ala	Asn	Leu	Ser	Ser	Val	Leu	Ser	Leu	Phe	Ala	Pro	Phe	Lys	Glu	Cys
			85						90					95	
Asp	Leu	Val	Gly	Leu	Glu	Lys	Ile	Glu	Pro	Ile	Leu	Asn	Ile	Leu	Ser
			100					105					110		
Gln	Thr	Gln	Thr	Asn	Ala	Leu	Lys	Glu	Leu	Gln	Lys	His	Ser	Ala	Ser
			115				120					125			
Leu	Leu	Phe	Gly	Asp	Thr	Gly	Ser	Gly	Lys	Thr	Glu	Ile	Tyr	Met	His
	130					135					140				
Ala	Ile	Ala	Gln	Thr	Leu	Glu	Gln	Lys	Lys	Ser	Ala	Leu	Leu	Leu	Val
145					150					155					160
Pro	Glu	Ile	Ala	Leu	Thr	Pro	Gln	Met	Gln	Gln	Arg	Leu	Lys	Arg	Val
				165					170					175	
Phe	Lys	Glu	Asn	Leu	Gly	Leu	Trp	His	Ser	Lys	Leu	Ser	Gln	Asn	Gln
			180					185					190		
Lys	Lys	Gln	Phe	Leu	Glu	Lys	Leu	Tyr	Ser	Gln	Glu	Ile	Lys	Leu	Val
		195					200					205			
Val	Gly	Thr	Arg	Ser	Ala	Leu	Phe	Leu	Pro	Leu	Lys	Glu	Leu	Gly	Leu
	210					215						220			
Ile	Ile	Val	Asp	Glu	Glu	His	Asp	Phe	Ser	Tyr	Lys	Ser	His	Gln	Ser
225					230					235					240
Pro	Met	Tyr	Asn	Ala	Arg	Asp	Leu	Cys	Leu	Tyr	Leu	Ser	His	Lys	Phe
				245					250					255	
Pro	Ile	Gln	Val	Ile	Leu	Gly	Ser	Ala	Thr	Pro	Ser	Leu	Asn	Ser	Tyr
			260					265					270		
Lys	Arg	Phe	Lys	Asp	Lys	Ala	Leu	Val	Arg	Leu	Lys	Gly	Arg	Tyr	Thr
		275					280					285			
Pro	Thr	Gln	Lys	Asn	Ile	Ile	Phe	Glu	Lys	Thr	Glu	Arg	Phe	Ile	Thr
	290					295					300				
Pro	Lys	Leu	Leu	Glu	Ala	Leu	Gln	Gln	Val	Leu	Asp	Lys	Asn	Glu	Gln

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305	Ala	Ile	Ile	Phe	Val	Pro	Thr	Arg	Ala	Asn	Phe	Lys	Thr	Leu	Leu	Cys
					325					330						335
Gln	Ser	Cys	Tyr	Lys	Ser	Val	Gln	Cys	Pro	Phe	Cys	Ser	Val	Asn	Met	
				340					345					350		
Ser	Leu	His	Leu	Lys	Thr	Asn	Lys	Leu	Met	Cys	His	Tyr	Cys	His	Phe	
		355					360				365					
Ser	Ser	Pro	Ile	Pro	Lys	Ile	Cys	Ser	Ala	Cys	Gln	Ser	Glu	Val	Leu	
		370				375					380					
Val	Gly	Lys	Arg	Ile	Gly	Thr	Met	Gln	Val	Leu	Lys	Glu	Leu	Glu	Ser	
385					390					395					400	
Leu	Leu	Glu	Gly	Ala	Lys	Ile	Ala	Ile	Leu	Asp	Lys	Asp	His	Thr	Ser	
				405					410					415		
Thr	Gln	Lys	Lys	Leu	His	Asn	Ile	Leu	Asn	Asp	Phe	Asn	Ala	Gln	Lys	
				420					425					430		
Thr	Asn	Ile	Leu	Ile	Gly	Thr	Gln	Met	Ile	Ser	Lys	Gly	His	Asp	Tyr	
		435					440					445				
Ala	Lys	Val	Ser	Leu	Ala	Val	Val	Leu	Gly	Ile	Asp	Asn	Ile	Ile	Lys	
		450				455					460					
Ser	Asn	Ser	Tyr	Arg	Ala	Leu	Glu	Glu	Gly	Val	Ser	Leu	Leu	Tyr	Gln	
465					470					475					480	
Ile	Ala	Gly	Arg	Ser	Ala	Arg	Gln	Ile	Ser	Gly	Gln	Val	Phe	Ile	Gln	
				485					490					495		
Ser	Thr	Glu	Thr	Asp	Leu	Leu	Glu	Asn	Phe	Leu	Glu	Asp	Tyr	Glu	Asp	
			500					505					510			
Phe	Leu	Gln	Tyr	Glu	Leu	Gln	Glu	Arg	Cys	Glu	Leu	Tyr	Pro	Pro	Phe	
		515					520					525				
Ser	Arg	Leu	Cys	Leu	Leu	Glu	Phe	Lys	His	Lys	Asn	Glu	Glu	Lys	Ala	
	530					535					540					
Gln	Gln	Leu	Ser	Leu	Lys	Ala	Ser	Gln	Thr	Leu	Ser	Ser	Cys	Leu	Glu	
545					550					555					560	
Lys	Gly	Val	Thr	Leu	Ser	Asn	Phe	Lys	Ala	Pro	Ile	Glu	Lys	Ile	Ala	
				565					570					575		
Ser	Ser	Tyr	Arg	Tyr	Leu	Ile	Leu	Leu	Arg	Ser	Lys	Asn	Pro	Leu	Ser	
			580					585				590				
Leu	Ile	Lys	Ser	Val	His	Ala	Phe	Leu	Lys	Ser	Ala	Pro	Ser	Ile	Pro	
		595				600						605				
Cys	Ser	Val	Asn	Met	Asp	Pro	Val	Asp	Ile	Phe						
	610					615										

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 <211> 2438  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (82)...(2373)

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gagagtgttg gagagctttt a atg aaa ctg agc att aat gat ttg aat gtt	111
Met Lys Leu Ser Ile Asn Asp Leu Asn Val	
1 5 10	
ttt gtc aat acg cct aaa gat ata gcc aaa ctc tgt gag gat ttg agt	159
Phe Val Asn Thr Pro Lys Asp Ile Ala Lys Leu Cys Glu Asp Leu Ser	
15 20 25	





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	495	500	505	
ttt gaa gtt tta gaa gat ccc cta gaa ttg caa aac cct atc aca acg				1647
Phe Glu Val Leu Glu Asp Pro Leu Glu Leu Gln Asn Pro Ile Thr Thr	510	515	520	
gag tta aac acc cta agg acg agt ctt gtt tgc ggg ctt tta gac gcc				1695
Glu Leu Asn Thr Leu Arg Thr Ser Leu Val Cys Gly Leu Leu Asp Ala	525	530	535	
agt tta agg aat aaa aat tta ggg ttt aaa agc ata gcc ctt tat gaa				1743
Ser Leu Arg Asn Lys Asn Leu Gly Phe Lys Ser Ile Ala Leu Tyr Glu	540	545	550	
aag ggg agc gtg tat aac tct aaa aga gaa gaa atc caa aaa cta ggc				1791
Lys Gly Ser Val Tyr Asn Ser Lys Arg Glu Glu Ile Gln Lys Leu Gly	555	560	565	570
ttt tta ata agc ggc ttg caa aaa aaa gaa agc tac cct gat act aag				1839
Phe Leu Ile Ser Gly Leu Gln Lys Lys Glu Ser Tyr Pro Asp Thr Lys	575	580	585	
ggc aag gct tgg gat ttt tac tct ttt gcc gaa tgc gtt tca aaa gtt				1887
Gly Lys Ala Trp Asp Phe Tyr Ser Phe Ala Glu Cys Val Ser Lys Val	590	595	600	
ata ggg gat ttc agc ttg gaa aaa cta acc act caa acc ccc att aac				1935
Ile Gly Asp Phe Ser Leu Glu Lys Leu Thr Thr Gln Thr Pro Ile Asn	605	610	615	
cac ccc tac cag agc gct aaa atc att caa aat cat gaa atc ata ggc				1983
His Pro Tyr Gln Ser Ala Lys Ile Ile Gln Asn His Glu Ile Ile Gly	620	625	630	
gtg atc gct aaa atc cac cct aaa gtg atc cag gaa ttg gat ttg ttt				2031
Val Ile Ala Lys Ile His Pro Lys Val Ile Gln Glu Leu Asp Leu Phe	635	640	645	650
gaa agc tat tac gct gag ata gac gct ttt aaa ctc aaa cgc cct gct				2079
Glu Ser Tyr Tyr Ala Glu Ile Asp Ala Phe Lys Leu Lys Arg Pro Ala	655	660	665	
atg cta tta aaa ccc ttt agc att tat cct agc agt gtt agg gat ttg				2127
Met Leu Leu Lys Pro Phe Ser Ile Tyr Pro Ser Ser Val Arg Asp Leu	670	675	680	
act ctc atc att gat gag aat acc gct ttt agt ggg att aaa aaa gcc				2175
Thr Leu Ile Ile Asp Glu Asn Thr Ala Phe Ser Gly Ile Lys Lys Ala	685	690	695	
cta aag gac gct caa atc cct aat tta agc gag att cta ccc ctt gat				2223
Leu Lys Asp Ala Gln Ile Pro Asn Leu Ser Glu Ile Leu Pro Leu Asp	700	705	710	
att ttt aaa gaa agt aat aat tcc ata gcc tta agc gtg cgt tgc gtg				2271
Ile Phe Lys Glu Ser Asn Asn Ser Ile Ala Leu Ser Val Arg Cys Val	715	720	725	730
atc cat tct tta gaa aaa acc ctg aat gat gaa gag gtc aat tca gcc				2319



Ile His Ser Leu Glu Lys Thr Leu Asn Asp Glu Glu Val Asn Ser Ala  
735 740 745

gtg caa aaa gca ctt gaa att tta gaa aaa gaa ttt aac gcc cgc ctt 2367  
Val Gln Lys Ala Leu Glu Ile Leu Glu Lys Glu Phe Asn Ala Arg Leu  
750 755 760

aaa gga taatataaag gataatatgt gatagagctt gacattaacg ctagcgataa 2423  
Lys Gly

atcgctctca cacag 2438

<210> 328  
<211> 764  
<212> PRT  
<213> Helicobacter pylori

<400> 328  
Met Lys Leu Ser Ile Asn Asp Leu Asn Val Phe Val Asn Thr Pro Lys  
1 5 10 15  
Asp Ile Ala Lys Leu Cys Glu Asp Leu Ser Arg Leu Gly Leu Glu Val  
20 25 30  
Glu Ser Cys Ile Pro Cys Ile Ala Pro Lys Asn Val Val Val Gly Lys  
35 40 45  
Ile Leu Glu Lys Ala Pro His Lys Asn Ala Glu Lys Leu Ser Val Cys  
50 55 60  
Gln Val Asp Val Gly Lys Glu Val Leu Gln Ile Val Cys Gly Ala Lys  
65 70 75 80  
Asn Val Ala Pro Asn Gln Phe Val Pro Val Ala Leu Asn Gly Ala Leu  
85 90 95  
Ile Gly Ser Thr Thr Ile Ala Lys Thr Glu Leu Arg Gly Val Glu Ser  
100 105 110  
His Gly Met Ile Cys Ser Ser Ile Glu Leu Gly Phe Pro Lys Ile Asn  
115 120 125  
Asp Gly Ile Leu Glu Leu Asp Glu Ser Val Gly Glu Leu Val Leu Gly  
130 135 140  
Lys Glu Leu Asn Glu Tyr Ala Pro Phe Asn Thr His Val Leu Glu Ile  
145 150 155 160  
Ser Leu Thr Pro Asn Arg Gly Asp Cys Leu Ser Val Leu Gly Ile Ala  
165 170 175  
Arg Glu Ile Ser Ala Phe Tyr His Thr Pro Leu Lys Pro Ile Lys Ala  
180 185 190  
Leu Asn Phe Thr Pro Lys Ser Gly Leu Ile Thr Leu Ser Ala Gly Glu  
195 200 205  
Asn Ile Glu Ser His Leu Ala Tyr Tyr Leu Ile Cys Asn His Ser Leu  
210 215 220  
Lys Thr Pro Leu Asn Ile Lys Leu Ser Leu Ala His Asn Asn Ala Leu  
225 230 235 240  
Ser Glu Asn Asp Leu Asn Asn Phe Ile Glu Phe Ser Thr His Phe Ser  
245 250 255  
Gly Val Ile Met Asn Ala Tyr Ser Leu Asn Thr Thr Pro Met Asp Leu  
260 265 270  
Ser Val Lys Asn Asp Glu Asn Asn Leu Glu Ser Val Tyr Ile Asn His  
275 280 285  
Gln Lys Arg Ser Thr Ile Ala Ile Lys His Gln Val Gln Lys Asp Leu  
290 295 300  
Ser Glu Cys Leu Leu Leu Glu Ala Ser Tyr Thr Asp Pro Ile Ser Leu  
305 310 315 320

106290.E165650

106290-ET5660

Ser	Leu	Lys	Leu	His	Ala	Leu	Lys	Asp	Lys	Thr	Leu	Gln	Lys	Asp	Asn	
				325					330					335		
Ala	Leu	Ile	Tyr	Arg	Ser	Ala	Arg	Gly	Ser	Asn	Pro	Asn	Leu	Ser	Asp	
			340					345					350			
Gly	Leu	Asn	Phe	Leu	Ser	Ala	His	Leu	Lys	Ala	Thr	Ile	Leu	Glu	Ser	
		355					360					365				
Lys	Gln	Thr	Glu	His	Ser	Leu	Lys	Asp	Arg	Thr	Leu	Thr	Phe	Gln	Leu	
	370					375					380					
Glu	Asp	Ile	Thr	Glu	Ile	Leu	Gly	Leu	Ala	Val	Glu	Lys	Glu	Lys	Ile	
385					390					395					400	
Gln	Gly	Ile	Leu	Lys	Asn	Leu	Gly	Phe	Lys	Val	Ser	Val	Lys	Glu	Pro	
				405				410						415		
Asn	Ser	Lys	Pro	Gln	Ile	Leu	Glu	Val	Ile	Ala	Pro	Asn	Phe	Arg	His	
			420					425					430			
Asp	Ile	Lys	Thr	Ile	Gln	Asp	Ile	Ala	Glu	Glu	Ile	Leu	Arg	Phe	Val	
		435					440					445				
Gly	Ile	Asp	Asn	Leu	Val	Ser	Lys	Pro	Leu	His	Cys	Val	Ser	Ser	Lys	
	450					455					460					
Asn	Ser	Asn	Pro	Asn	Tyr	Asp	Thr	His	Arg	Phe	Phe	Glu	Asn	Leu	Lys	
465					470					475					480	
His	Lys	Ala	Leu	Ala	Cys	Gly	Phe	Lys	Glu	Val	Ile	His	Tyr	Val	Phe	
				485					490					495		
Tyr	Ser	Lys	Glu	Lys	Gln	Gln	Lys	Leu	Gly	Phe	Glu	Val	Leu	Glu	Asp	
			500					505					510			
Pro	Leu	Glu	Leu	Gln	Asn	Pro	Ile	Thr	Thr	Glu	Leu	Asn	Thr	Leu	Arg	
		515					520					525				
Thr	Ser	Leu	Val	Cys	Gly	Leu	Leu	Asp	Ala	Ser	Leu	Arg	Asn	Lys	Asn	
	530					535					540					
Leu	Gly	Phe	Lys	Ser	Ile	Ala	Leu	Tyr	Glu	Lys	Gly	Ser	Val	Tyr	Asn	
545					550					555					560	
Ser	Lys	Arg	Glu	Glu	Ile	Gln	Lys	Leu	Gly	Phe	Leu	Ile	Ser	Gly	Leu	
				565					570					575		
Gln	Lys	Lys	Glu	Ser	Tyr	Pro	Asp	Thr	Lys	Gly	Lys	Ala	Trp	Asp	Phe	
			580					585					590			
Tyr	Ser	Phe	Ala	Glu	Cys	Val	Ser	Lys	Val	Ile	Gly	Asp	Phe	Ser	Leu	
		595					600					605				
Glu	Lys	Leu	Thr	Thr	Gln	Thr	Pro	Ile	Asn	His	Pro	Tyr	Gln	Ser	Ala	
	610					615					620					
Lys	Ile	Ile	Gln	Asn	His	Glu	Ile	Ile	Gly	Val	Ile	Ala	Lys	Ile	His	
625					630					635					640	
Pro	Lys	Val	Ile	Gln	Glu	Leu	Asp	Leu	Phe	Glu	Ser	Tyr	Tyr	Ala	Glu	
				645					650					655		
Ile	Asp	Ala	Phe	Lys	Leu	Lys	Arg	Pro	Ala	Met	Leu	Leu	Lys	Pro	Phe	
		660						665					670			
Ser	Ile	Tyr	Pro	Ser	Ser	Val	Arg	Asp	Leu	Thr	Leu	Ile	Ile	Asp	Glu	
		675					680					685				
Asn	Thr	Ala	Phe	Ser	Gly	Ile	Lys	Lys	Ala	Leu	Lys	Asp	Ala	Gln	Ile	
	690					695					700					
Pro	Asn	Leu	Ser	Glu	Ile	Leu	Pro	Leu	Asp	Ile	Phe	Lys	Glu	Ser	Asn	
705					710					715					720	
Asn	Ser	Ile	Ala	Leu	Ser	Val	Arg	Cys	Val	Ile	His	Ser	Leu	Glu	Lys	
			725						730					735		
Thr	Leu	Asn	Asp	Glu	Glu	Val	Asn	Ser	Ala	Val	Gln	Lys	Ala	Leu	Glu	
		740						745					750			
Ile	Leu	Glu	Lys	Glu	Phe	Asn	Ala	Arg	Leu	Lys	Gly					
		755					760									

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<211> 1097

<212> DNA  
<213> Helicobacter pylori

<220>  
<221> CDS  
<222> (492)...(1040)

<400> 329

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acaccttaat	agagcgatta	gaaaagggtta	ctaataagcaa	agagttagaa	gaagcgcgct	120
tgaatgcttt	gggtaaaaaaa	gggggtttttg	cggataaatt	caaccagctc	aaacatctga	180
acggcgaga	aaaaaacgcc	tttgctaaag	aaatccacca	ttataaaca	gcgtttgaaa	240
aagcctttga	atggaaaaaa	aaggctatta	tagagcttga	attagaagaa	cgcttgaaaa	300
aagaaaaaat	tgatgtgagc	ttgtttaacg	ctatcaaac	aagctcttct	caccctttaa	360
actacactaa	aaataaaaatc	attgaatttt	tcacccatt	aggatacaag	cttgaaatcg	420
gctctttagt	ggaagatgat	ttccataatt	tcagcgcttt	aaacttgccc	ccttaccatc	480
ctgcaagaga	c atg caa gac act ttt	tat ttt aaa	gat cac aag ctt tta			530
	Met Gln Asp Thr Phe	Tyr Phe Lys	Asp His Lys Leu Leu			
	1	5	10			
agg acc cac act tcg ccc gtg caa atc cac acc atg caa gaa caa acc						578
Arg Thr His Thr Ser Pro Val Gln Ile His Thr Met Gln Glu Gln Thr						
15	20	25				
cca ccc att aag atg att tgt tta ggc gaa acc ttt agg cgc gat tat						626
Pro Pro Ile Lys Met Ile Cys Leu Gly Glu Thr Phe Arg Arg Asp Tyr						
30	35	40			45	
gat ttg acc cac acg ccc atg ttc cac caa att gaa ggg ctt gtc gtg						674
Asp Leu Thr His Thr Pro Met Phe His Gln Ile Glu Gly Leu Val Val						
50	55	60				
gat caa aaa ggg aat atc cgt ttc aca cat tta aaa ggt gtg atc gaa						722
Asp Gln Lys Gly Asn Ile Arg Phe Thr His Leu Lys Gly Val Ile Glu						
65	70	75				
gac ttt ttg cat tat ttc ttt ggg ggc gtg aag tta agg tgg cgc tct						770
Asp Phe Leu His Tyr Phe Phe Gly Gly Val Lys Leu Arg Trp Arg Ser						
80	85	90				
agc ttt ttc cct ttc aca gag cca agc gct gaa gtg gat att agt tgc						818
Ser Phe Phe Pro Phe Thr Glu Pro Ser Ala Glu Val Asp Ile Ser Cys						
95	100	105				
gtg ttt tgc aag caa gaa ggc tgt agg gtt tgc tcg cac aca ggc tgg						866
Val Phe Cys Lys Gln Glu Gly Cys Arg Val Cys Ser His Thr Gly Trp						
110	115	120			125	
tta gaa gtg ttg ggc tgt ggc atg gtc aat aat gcg gtg ttt gaa gcc						914
Leu Glu Val Leu Gly Cys Gly Met Val Asn Asn Ala Val Phe Glu Ala						
130	135	140				
ata ggg tat gag aat gtg agc ggg ttt gct ttt ggc atg ggg att gaa						962
Ile Gly Tyr Glu Asn Val Ser Gly Phe Ala Phe Gly Met Gly Ile Glu						
145	150	155				
aga tta gcc atg ctg act tgc cag atc aat gat ttg cgc agt ttc ttt						1010
Arg Leu Ala Met Leu Thr Cys Gln Ile Asn Asp Leu Arg Ser Phe Phe						
160	165	170				

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gaa act gat ttg aga gtg ttg gag agc ttt taatgaaact gagcattaat 1060  
 Glu Thr Asp Leu Arg Val Leu Glu Ser Phe  
 175 180

gatttgaatg tttttgtcaa tacgcctaaa gatatag 1097

<210> 330  
 <211> 183  
 <212> PRT  
 <213> Helicobacter pylori

<400> 330  
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 1 5 10 15  
 Thr Ser Pro Val Gln Ile His Thr Met Gln Glu Gln Thr Pro Pro Ile  
 20 25 30  
 Lys Met Ile Cys Leu Gly Glu Thr Phe Arg Arg Asp Tyr Asp Leu Thr  
 35 40 45  
 His Thr Pro Met Phe His Gln Ile Glu Gly Leu Val Val Asp Gln Lys  
 50 55 60  
 Gly Asn Ile Arg Phe Thr His Leu Lys Gly Val Ile Glu Asp Phe Leu  
 65 70 75 80  
 His Tyr Phe Phe Gly Gly Val Lys Leu Arg Trp Arg Ser Ser Phe Phe  
 85 90 95  
 Pro Phe Thr Glu Pro Ser Ala Glu Val Asp Ile Ser Cys Val Phe Cys  
 100 105 110  
 Lys Gln Glu Gly Cys Arg Val Cys Ser His Thr Gly Trp Leu Glu Val  
 115 120 125  
 Leu Gly Cys Gly Met Val Asn Asn Ala Val Phe Glu Ala Ile Gly Tyr  
 130 135 140  
 Glu Asn Val Ser Gly Phe Ala Phe Gly Met Gly Ile Glu Arg Leu Ala  
 145 150 155 160  
 Met Leu Thr Cys Gln Ile Asn Asp Leu Arg Ser Phe Phe Glu Thr Asp  
 165 170 175  
 Leu Arg Val Leu Glu Ser Phe  
 180

<210> 331  
 <211> 517  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (51)...(464)

<400> 331  
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 Met Lys  
 1

aaa att gat gat atg aga cac gga aga cat tgt gtt ttt tta atg cat 104  
 Lys Ile Asp Asp Met Arg His Gly Arg His Cys Val Phe Leu Met His  
 5 10 15

gtg cat ttt gta ttt gtt act aaa tac agg cgt tca gca ttc aat aag 152  
 Val His Phe Val Phe Val Thr Lys Tyr Arg Arg Ser Ala Phe Asn Lys  
 20 25 30

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gaa gtg ata gat ttt tta gga tgc gtg ttt gcc aaa gtg tgt aag gac 200  
 Glu Val Ile Asp Phe Leu Gly Ser Val Phe Ala Lys Val Cys Lys Asp  
 35 40 45 50

ttt gag agc gaa ttg gta gaa ttt gat ggg gag agc gat cat gtg cat 248  
 Phe Glu Ser Glu Leu Val Glu Phe Asp Gly Glu Ser Asp His Val His  
 55 60 65

ttg ctt atc aac tac cct cca aaa gtg agc gtg agt aag tta gtt aat 296  
 Leu Leu Ile Asn Tyr Pro Pro Lys Val Ser Val Ser Lys Leu Val Asn  
 70 75 80

tct tta aaa ggc gtt agc agt cgt ttg act aga caa cac cat ttc aaa 344  
 Ser Leu Lys Gly Val Ser Ser Arg Leu Thr Arg Gln His His Phe Lys  
 85 90 95

agc gtt gaa gct agt ttg tgg ggg aag cat tta tgg tgc cct agt tat 392  
 Ser Val Glu Ala Ser Leu Trp Gly Lys His Leu Trp Ser Pro Ser Tyr  
 100 105 110

ttc gct ggg agt tgt ggg gac gcg cct tta gag atg att aag caa tac 440  
 Phe Ala Gly Ser Cys Gly Asp Ala Pro Leu Glu Met Ile Lys Gln Tyr  
 115 120 125 130

ata caa gat caa gaa aca ccg cat taaattagct aactttgatt tttaagtaga 494  
 Ile Gln Asp Gln Glu Thr Pro His  
 135

acgcgctaaa aagcgaatgg atc 517

<210> 332  
 <211> 138  
 <212> PRT  
 <213> Helicobacter pylori

<400> 332  
 Met Lys Lys Ile Asp Asp Met Arg His Gly Arg His Cys Val Phe Leu  
 1 5 10 15  
 Met His Val His Phe Val Phe Val Thr Lys Tyr Arg Arg Ser Ala Phe  
 20 25 30  
 Asn Lys Glu Val Ile Asp Phe Leu Gly Ser Val Phe Ala Lys Val Cys  
 35 40 45  
 Lys Asp Phe Glu Ser Glu Leu Val Glu Phe Asp Gly Glu Ser Asp His  
 50 55 60  
 Val His Leu Leu Ile Asn Tyr Pro Pro Lys Val Ser Val Ser Lys Leu  
 65 70 75 80  
 Val Asn Ser Leu Lys Gly Val Ser Ser Arg Leu Thr Arg Gln His His  
 85 90 95  
 Phe Lys Ser Val Glu Ala Ser Leu Trp Gly Lys His Leu Trp Ser Pro  
 100 105 110  
 Ser Tyr Phe Ala Gly Ser Cys Gly Asp Ala Pro Leu Glu Met Ile Lys  
 115 120 125  
 Gln Tyr Ile Gln Asp Gln Glu Thr Pro His  
 130 135

<210> 333  
 <211> 1786  
 <212> DNA

080501Z FEB 67

<221> CDS

<222> (51) ... (1733)

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Met Gln															
1															
gaa gtc cat gat tat ggg att aaa ttt tgg agc aat aac gaa ttt aag															104
Glu Val His Asp Tyr Gly Ile Lys Phe Trp Ser Asn Asn Glu Phe Lys															
5 10 15															
ata gaa aaa ggc ttg gtt aaa gtc tgt cat ggt aaa aac ccc tcg ctt															152
Ile Glu Lys Gly Leu Val Lys Val Cys His Gly Lys Asn Pro Ser Leu															
20 25 30															
tta gaa atc gtt caa agc gtg cgc gat aag ggc tat aga gga cct ttg															200
Leu Glu Ile Val Gln Ser Val Arg Asp Lys Gly Tyr Arg Gly Pro Leu															
35 40 45 50															
ttg gtg cga ttc ccc cat ttg gtg caa aaa caa atc aaa agc ctg ttt															248
Leu Val Arg Phe Pro His Leu Val Gln Lys Gln Ile Lys Ser Leu Phe															
55 60 65															
gat gcg ttt tct tca gcg att aaa gag tat caa tac agc ggg gct ttt															296
Asp Ala Phe Ser Ser Ala Ile Lys Glu Tyr Gln Tyr Ser Gly Ala Phe															
70 75 80															
aag gcg gtt ttc cct tta aaa gtc aat caa atg ccc tcg ttt gtt ttc															344
Lys Ala Val Phe Pro Leu Lys Val Asn Gln Met Pro Ser Phe Val Phe															
85 90 95															
cct tta gtg cag ggg gct aag ggt ttg aat tac gga tta gag gct ggg															392
Pro Leu Val Gln Gly Ala Lys Gly Leu Asn Tyr Gly Leu Glu Ala Gly															
100 105 110															
agc aag tct gaa ctc atc atc gca atg agt tac act aac cct aaa gcc															440
Ser Lys Ser Glu Leu Ile Ile Ala Met Ser Tyr Thr Asn Pro Lys Ala															
115 120 125 130															
cct atc acc gtg aat ggc ttt aaa gac aaa gaa atg att gag ctt ggc															488
Pro Ile Thr Val Asn Gly Phe Lys Asp Lys Glu Met Ile Glu Leu Gly															
135 140 145															
ttt atc gct aaa agc atg cag cat gag atc act tta acg att gag ggt															536
Phe Ile Ala Lys Ser Met Gln His Glu Ile Thr Leu Thr Ile Glu Gly															
150 155 160															
ttg aat gaa ttg aaa acc att atc gcc gtg gct aaa caa aac gag ttt															584
Leu Asn Glu Leu Lys Thr Ile Ile Ala Val Ala Lys Gln Asn Glu Phe															
165 170 175															
tta gcc tgc cct aaa att ggc atc cgc atc cgt ttg cac agc act ggc															632
Leu Ala Cys Pro Lys Ile Gly Ile Arg Ile Arg Leu His Ser Thr Gly															
180 185 190															

act ggc gtt tgg gca aag agt ggg ggg atc aat tct aaa ttt ggt ctt	680
Thr Gly Val Trp Ala Lys Ser Gly Gly Ile Asn Ser Lys Phe Gly Leu	
195 200 205 210	
agc agc act gaa gtt tta gag gcg atg cgc ctt tta gaa gaa aac gac	728
Ser Ser Thr Glu Val Leu Glu Ala Met Arg Leu Leu Glu Glu Asn Asp	
215 220 225	
ttg tta gag cat ttc cac atg ata cat ttc cat ata ggc tct caa atc	776
Leu Leu Glu His Phe His Met Ile His Phe His Ile Gly Ser Gln Ile	
230 235 240	
agc gat att tcg ccc tta aaa aag gct tta aga gaa gcg ggt aac ttg	824
Ser Asp Ile Ser Pro Leu Lys Lys Ala Leu Arg Glu Ala Gly Asn Leu	
245 250 255	
tat gca gaa ttg cgt aaa atg ggc gct aaa aat ctt aat agc gtg aat	872
Tyr Ala Glu Leu Arg Lys Met Gly Ala Lys Asn Leu Asn Ser Val Asn	
260 265 270	
att gga ggg ggg tta gcc gta gaa tac acc caa cac aag cac cac caa	920
Ile Gly Gly Gly Leu Ala Val Glu Tyr Thr Gln His Lys His His Gln	
275 280 285 290	
gac aaa aac tac act tta gag gaa ttc agc gct gat gtg gtg ttt tta	968
Asp Lys Asn Tyr Thr Leu Glu Glu Phe Ser Ala Asp Val Val Phe Leu	
295 300 305	
ttg aga gaa att gtg aaa aat aag cag gaa atc gag ccg gac att ttc	1016
Leu Arg Glu Ile Val Lys Asn Lys Gln Glu Ile Glu Pro Asp Ile Phe	
310 315 320	
att gaa tca ggc cgt tat att tcc gct aac cat gcc gtt tta gtg gcc	1064
Ile Glu Ser Gly Arg Tyr Ile Ser Ala Asn His Ala Val Leu Val Ala	
325 330 335	
ccg gtg tta gaa ttg ttt tcg cat gaa tac aat gaa aaa tcc cta aaa	1112
Pro Val Leu Glu Leu Phe Ser His Glu Tyr Asn Glu Lys Ser Leu Lys	
340 345 350	
atc aaa gaa aat aat aac ccc cct ttg att gat gaa atg cta gac ttg	1160
Ile Lys Glu Asn Asn Asn Pro Pro Leu Ile Asp Glu Met Leu Asp Leu	
355 360 365 370	
ctc gct aat atc aat gaa aaa aac gcc att gaa tac ttg cat gat agt	1208
Leu Ala Asn Ile Asn Glu Lys Asn Ala Ile Glu Tyr Leu His Asp Ser	
375 380 385	
ttt gat cac acc gag tcg cta ttc acg ctt ttt gat ctg ggc tat att	1256
Phe Asp His Thr Glu Ser Leu Phe Thr Leu Phe Asp Leu Gly Tyr Ile	
390 395 400	
gat ttg att gac agg agc aac act gaa gtt tta gcc cat ttg atc gtc	1304
Asp Leu Ile Asp Arg Ser Asn Thr Glu Val Leu Ala His Leu Ile Val	
405 410 415	
aaa aaa gcg gtg caa ttg ctt tat gtt aag gat cat aac gat att tta	1352
Lys Lys Ala Val Gln Leu Leu Tyr Val Lys Asp His Asn Asp Ile Leu	
420 425 430	

09095913 062901

cgc att caa gag cag gtc caa gag cgc tat tta ttg aat tgc tgc ttt 1400  
Arg Ile Gln Glu Gln Val Gln Glu Arg Tyr Leu Leu Asn Cys Ser Phe  
435 440 445 450

ttc caa agc ttg ccg gat tat tgg ggc ttg aga cag aat ttc ccg gtc 1448  
Phe Gln Ser Leu Pro Asp Tyr Trp Gly Leu Arg Gln Asn Phe Pro Val  
455 460 465

atg ccc ttg aat aaa tta gat gaa aag ccc acc agg agt gcg agc ttg 1496  
Met Pro Leu Asn Lys Leu Asp Glu Lys Pro Thr Arg Ser Ala Ser Leu  
470 475 480

tgg gat att act tgc gat agc gat ggg gaa atc gct ttt gat tcc acg 1544  
Trp Asp Ile Thr Cys Asp Ser Asp Gly Glu Ile Ala Phe Asp Ser Thr  
485 490 495

aag ccc ttg ttt ttg cac gat ata gat ata gat gaa gaa gaa tac ttt 1592  
Lys Pro Leu Phe Leu His Asp Ile Asp Ile Asp Glu Glu Glu Tyr Phe  
500 505 510

tta gcg ttc ttt tta gtg gga gcg tat caa gaa gtt tta ggc atg aaa 1640  
Leu Ala Phe Phe Leu Val Gly Ala Tyr Gln Glu Val Leu Gly Met Lys  
515 520 525 530

cac aat tta ttc acg cac cta cgg aat tta gcg tgg ttt ttg atg aaa 1688  
His Asn Leu Phe Thr His Leu Arg Asn Leu Ala Trp Phe Leu Met Lys  
535 540 545

aag gcg att atg aag tgg aag ata ttt gtg aag ccc aaa cga ttt 1733  
Lys Ala Ile Met Lys Trp Lys Ile Phe Val Lys Pro Lys Arg Phe  
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<213> Helicobacter pylori

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Ser Leu Leu Glu Ile Val Gln Ser Val Arg Asp Lys Gly Tyr Arg Gly  
35 40 45  
Pro Leu Leu Val Arg Phe Pro His Leu Val Gln Lys Gln Ile Lys Ser  
50 55 60  
Leu Phe Asp Ala Phe Ser Ser Ala Ile Lys Glu Tyr Gln Tyr Ser Gly  
65 70 75 80  
Ala Phe Lys Ala Val Phe Pro Leu Lys Val Asn Gln Met Pro Ser Phe  
85 90 95  
Val Phe Pro Leu Val Gln Gly Ala Lys Gly Leu Asn Tyr Gly Leu Glu  
100 105 110  
Ala Gly Ser Lys Ser Glu Leu Ile Ala Met Ser Tyr Thr Asn Pro  
115 120 125  
Lys Ala Pro Ile Thr Val Asn Gly Phe Lys Asp Lys Glu Met Ile Glu  
130 135 140



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Leu	Gly	Phe	Ile	Ala	Lys	Ser	Met	Gln	His	Glu	Ile	Thr	Leu	Thr	Ile
145					150					155					160
Glu	Gly	Leu	Asn	Glu	Leu	Lys	Thr	Ile	Ile	Ala	Val	Ala	Lys	Gln	Asn
			165						170						175
Glu	Phe	Leu	Ala	Cys	Pro	Lys	Ile	Gly	Ile	Arg	Ile	Arg	Leu	His	Ser
			180					185					190		
Thr	Gly	Thr	Gly	Val	Trp	Ala	Lys	Ser	Gly	Gly	Ile	Asn	Ser	Lys	Phe
		195					200					205			
Gly	Leu	Ser	Ser	Thr	Glu	Val	Leu	Glu	Ala	Met	Arg	Leu	Leu	Glu	Glu
	210					215				220					
Asn	Asp	Leu	Leu	Glu	His	Phe	His	Met	Ile	His	Phe	His	Ile	Gly	Ser
225					230					235					240
Gln	Ile	Ser	Asp	Ile	Ser	Pro	Leu	Lys	Lys	Ala	Leu	Arg	Glu	Ala	Gly
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Asn	Leu	Tyr	Ala	Glu	Leu	Arg	Lys	Met	Gly	Ala	Lys	Asn	Leu	Asn	Ser
			260					265					270		
Val	Asn	Ile	Gly	Gly	Gly	Leu	Ala	Val	Glu	Tyr	Thr	Gln	His	Lys	His
		275					280					285			
His	Gln	Asp	Lys	Asn	Tyr	Thr	Leu	Glu	Glu	Phe	Ser	Ala	Asp	Val	Val
	290					295					300				
Phe	Leu	Leu	Arg	Glu	Ile	Val	Lys	Asn	Lys	Gln	Glu	Ile	Glu	Pro	Asp
305					310					315					320
Ile	Phe	Ile	Glu	Ser	Gly	Arg	Tyr	Ile	Ser	Ala	Asn	His	Ala	Val	Leu
			325					330							335
Val	Ala	Pro	Val	Leu	Glu	Leu	Phe	Ser	His	Glu	Tyr	Asn	Glu	Lys	Ser
			340					345					350		
Leu	Lys	Ile	Lys	Glu	Asn	Asn	Asn	Pro	Pro	Leu	Ile	Asp	Glu	Met	Leu
		355					360					365			
Asp	Leu	Leu	Ala	Asn	Ile	Asn	Glu	Lys	Asn	Ala	Ile	Glu	Tyr	Leu	His
	370					375					380				
Asp	Ser	Phe	Asp	His	Thr	Glu	Ser	Leu	Phe	Thr	Leu	Phe	Asp	Leu	Gly
385					390					395					400
Tyr	Ile	Asp	Leu	Ile	Asp	Arg	Ser	Asn	Thr	Glu	Val	Leu	Ala	His	Leu
			405						410						415
Ile	Val	Lys	Lys	Ala	Val	Gln	Leu	Leu	Tyr	Val	Lys	Asp	His	Asn	Asp
			420					425					430		
Ile	Leu	Arg	Ile	Gln	Glu	Gln	Val	Gln	Glu	Arg	Tyr	Leu	Leu	Asn	Cys
		435					440					445			
Ser	Phe	Phe	Gln	Ser	Leu	Pro	Asp	Tyr	Trp	Gly	Leu	Arg	Gln	Asn	Phe
	450					455					460				
Pro	Val	Met	Pro	Leu	Asn	Lys	Leu	Asp	Glu	Lys	Pro	Thr	Arg	Ser	Ala
465					470					475					480
Ser	Leu	Trp	Asp	Ile	Thr	Cys	Asp	Ser	Asp	Gly	Glu	Ile	Ala	Phe	Asp
			485						490						495
Ser	Thr	Lys	Pro	Leu	Phe	Leu	His	Asp	Ile	Asp	Ile	Asp	Glu	Glu	Glu
			500					505					510		
Tyr	Phe	Leu	Ala	Phe	Phe	Leu	Val	Gly	Ala	Tyr	Gln	Glu	Val	Leu	Gly
		515					520					525			
Met	Lys	His	Asn	Leu	Phe	Thr	His	Leu	Arg	Asn	Leu	Ala	Trp	Phe	Leu
	530					535					540				
Met	Lys	Lys	Ala	Ile	Met	Lys	Trp	Lys	Ile	Phe	Val	Lys	Pro	Lys	Arg
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Phe															

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 <213> Helicobacter pylori

0589413 066001

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		60					65					70					
ctt	tta	agt	gaa	atc	gtt	ata	gat	tct	aga	agt	tct	aaa	att	gcg	tta	352	
Leu	Leu	Ser	Glu	Ile	Val	Ile	Asp	Ser	Arg	Ser	Ser	Lys	Ile	Ala	Leu		
	75					80					85						
aac	cgc	cat	tat	gcc	tta	act	cgc	ttg	caa	tgg	tgc	gat	aga	acc	tta	400	
Asn	Arg	His	Tyr	Ala	Leu	Thr	Arg	Leu	Gln	Trp	Cys	Asp	Arg	Thr	Leu		
	90				95					100					105		
aga	cat	aat	ctc	caa	att	tta	gag	aga	ata	gga	ttt	cta	act	gct	ttt	448	
Arg	His	Asn	Leu	Gln	Ile	Leu	Glu	Arg	Ile	Gly	Phe	Leu	Thr	Ala	Phe		
				110					115					120			
aag	aac	aaa	aaa	ggg	tat	att	ttt	ttg	tct	atg	cat	gac	ttc	act	aaa	496	
Lys	Asn	Lys	Lys	Gly	Tyr	Ile	Phe	Leu	Ser	Met	His	Asp	Phe	Thr	Lys		
			125					130					135				
ata	gaa	aac	tac	gaa	cat	tca	ggg	ttg	aat	ggg	gag	agc	aat	tta	cct	544	
Ile	Glu	Asn	Tyr	Glu	His	Ser	Gly	Leu	Asn	Gly	Glu	Ser	Asn	Leu	Pro		
		140					145					150					
aat	agc	ttc	ttt	tta	gga	att	tgt	ggg	tat	ttg	aaa	aaa	ctc	ttc	aag	592	
Asn	Ser	Phe	Phe	Leu	Gly	Ile	Cys	Gly	Tyr	Leu	Lys	Lys	Leu	Phe	Lys		
	155					160					165						
aaa	tta	aaa	gat	aga	gca	ttc	agg	ctc	gca	aac	aag	cac	ggg	gta	ttc	640	
Lys	Leu	Lys	Asp	Arg	Ala	Phe	Arg	Leu	Ala	Asn	Lys	His	Gly	Val	Phe		
	170				175					180				185			
ttt	ttg	aaa	att	cct	aag	cat	ttt	caa	atg	caa	aac	ttt	aac	aat	att	688	
Phe	Leu	Lys	Ile	Pro	Lys	His	Phe	Gln	Met	Gln	Asn	Phe	Asn	Asn	Ile		
				190					195					200			
ttt	ttg	gag	ttt	gtg	tcg	gtt	aat	aat	cct	tgt	ttt	tct	tat	aga	ttg	736	
Phe	Leu	Glu	Phe	Val	Ser	Val	Asn	Asn	Pro	Cys	Phe	Ser	Tyr	Arg	Leu		
			205					210					215				
act	tat	gat	caa	ctt	gtt	ggg	aaa	aaa	att	cca	aat	atc	aag	tgc	tct	784	
Thr	Tyr	Asp	Gln	Leu	Val	Gly	Lys	Lys	Ile	Pro	Asn	Ile	Lys	Cys	Ser		
		220					225					230					
tac	caa	caa	gca	att	gta	aaa	aag	aat	atc	cat	aga	gca	tta	gat	gaa	832	
Tyr	Gln	Gln	Ala	Ile	Val	Lys	Lys	Asn	Ile	His	Arg	Ala	Leu	Asp	Glu		
	235					240					245						
cta	tct	ata	gat	aag	gaa	att	tta	gca	tca	taaagaagac	aaaggataaa					882	
Leu	Ser	Ile	Asp	Lys	Glu	Ile	Leu	Ala	Ser								
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<210> 338  
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 <213> Helicobacter pylori  
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          20          25          30
Arg Phe Ile Pro Phe Lys Phe Asp Lys Phe Gly Tyr Val Gly Cys Lys
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Leu Phe Lys Lys Ile Leu Asn Phe Pro Ser Asn Thr Thr Phe Phe Gly
          50          55          60
Gly Thr Gly Cys Lys Lys Leu Met Glu Leu Leu Ser Glu Ile Val Ile
65          70          75          80
Asp Ser Arg Ser Ser Lys Ile Ala Leu Asn Arg His Tyr Ala Leu Thr
          85          90          95
Arg Leu Gln Trp Cys Asp Arg Thr Leu Arg His Asn Leu Gln Ile Leu
          100          105          110
Glu Arg Ile Gly Phe Leu Thr Ala Phe Lys Asn Lys Lys Gly Tyr Ile
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Phe Leu Ser Met His Asp Phe Thr Lys Ile Glu Asn Tyr Glu His Ser
          130          135          140
Gly Leu Asn Gly Glu Ser Asn Leu Pro Asn Ser Phe Phe Leu Gly Ile
145          150          155          160
Cys Gly Tyr Leu Lys Lys Leu Phe Lys Lys Leu Lys Asp Arg Ala Phe
          165          170          175
Arg Leu Ala Asn Lys His Gly Val Phe Phe Leu Lys Ile Pro Lys His
          180          185          190
Phe Gln Met Gln Asn Phe Asn Asn Ile Phe Leu Glu Phe Val Ser Val
          195          200          205
Asn Asn Pro Cys Phe Ser Tyr Arg Leu Thr Tyr Asp Gln Leu Val Gly
          210          215          220
Lys Lys Ile Pro Asn Ile Lys Cys Ser Tyr Gln Gln Ala Ile Val Lys
225          230          235          240
Lys Asn Ile His Arg Ala Leu Asp Glu Leu Ser Ile Asp Lys Glu Ile
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Leu Ala Ser

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Leu Glu Glu Leu Tyr Ala Pro Asn His Ile Glu Arg Leu Lys Ala Arg
          5          10          15

agt ttt tta aga tcg att gct ttt ttt gat gat ttt agc gct tct ttt      152
Ser Phe Leu Arg Ser Ile Ala Phe Phe Asp Asp Phe Ser Ala Ser Phe
          20          25          30

gaa tac aga gat cta ttt agc gtt ttg gaa aat atc gtg caa ttt gat      200
Glu Tyr Arg Asp Leu Phe Ser Val Leu Glu Asn Ile Val Gln Phe Asp

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tat gaa aaa aag ccg tat aaa gat gat ttg tat ttt ttg tgc aaa ttt				248
Tyr Glu Lys Lys Pro Tyr Lys Asp Asp Leu Tyr Phe Leu Cys Lys Phe	55	60	65	
gtg gag cca gcc cta aag gct atc ttt agc aat cta aat acc aat atc				296
Val Glu Pro Ala Leu Lys Ala Ile Phe Ser Asn Leu Asn Thr Asn Ile	70	75	80	
tac cga aaa cat tta aaa atg cct tta gaa aag gct agg gaa ttt gac				344
Tyr Arg Lys His Leu Lys Met Pro Leu Glu Lys Ala Arg Glu Phe Asp	85	90	95	
gct aaa tgc gcg ttg gat tta gcc aag cga cca ggt cgt agt ttg aaa				392
Ala Lys Cys Ala Leu Asp Leu Ala Lys Arg Pro Gly Arg Ser Leu Lys	100	105	110	
gaa aag ttg tgc gac aat aaa gta ttg agc gtc aag cgt tat gtg aat				440
Glu Lys Leu Cys Asp Asn Lys Val Leu Ser Val Lys Arg Tyr Val Asn	115	120	125	130
gcc aat acg cat gaa aac agg ttt ctc aag cgt ttc att aaa gaa ctt				488
Ala Asn Thr His Glu Asn Arg Phe Leu Lys Arg Phe Ile Lys Glu Leu	135	140	145	
tta aga ata att cat tgg cgc gag ata gaa ttc caa cag gtt ttt gaa				536
Leu Arg Ile Ile His Trp Arg Glu Ile Glu Phe Gln Gln Val Phe Glu	150	155	160	
gag tta att ttc agc ata aca agt ttt tta aag aat gga gta gcc caa				584
Glu Leu Ile Phe Ser Ile Thr Ser Phe Leu Lys Asn Gly Val Ala Gln	165	170	175	
caa att gat gaa aaa caa gcc atc att cct aat aac ttg ttg cat ttt				632
Gln Ile Asp Glu Lys Gln Ala Ile Ile Pro Asn Asn Leu Leu His Phe	180	185	190	
gat aag cac tac aaa cgc att ttt aaa gcc cat gat tgg ctt tat gat				680
Asp Lys His Tyr Lys Arg Ile Phe Lys Ala His Asp Trp Leu Tyr Asp	195	200	205	210
ggt gtg ggg tca ttg atg aat ttg gat caa att ttc tat ttg gag tgt				728
Gly Val Gly Ser Leu Met Asn Leu Asp Gln Ile Phe Tyr Leu Glu Cys	215	220	225	
tta tac caa gcc caa ttt tat act tct aaa aac att gaa ccc acg cta				776
Leu Tyr Gln Ala Gln Phe Tyr Thr Ser Lys Asn Ile Glu Pro Thr Leu	230	235	240	
att aga aat gaa caa gat tta tac gcg cta att aaa aat agt ttt cca				824
Ile Arg Asn Glu Gln Asp Leu Tyr Ala Leu Ile Lys Asn Ser Phe Pro	245	250	255	
ata aaa gat tta tcg ttt gaa aag atg cgt tta aaa gcg aaa gag ttt				872
Ile Lys Asp Leu Ser Phe Glu Lys Met Arg Leu Lys Ala Lys Glu Phe	260	265	270	
ttt gaa aat gaa tta aga cag cct ata aat tta gat caa gaa att ccg				920

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Gln	Leu	Glu	Leu	Cys	Lys	Gly	Val	Tyr	Lys	Glu	Met	Tyr	Ile	Asp	Met	
				295					300					305		
ttt	agc	cct	gaa	cct	ttc	gct	ttg	tta	gtg	ggt	aat	ggc	aat	gaa	gaa	1016
Phe	Ser	Pro	Glu	Pro	Phe	Ala	Leu	Leu	Val	Gly	Asn	Gly	Asn	Glu	Glu	
			310					315					320			
aag	att	tta	aag	ctc	ccc	ctt	tta	gtc	aaa	aag	cag	gag	aat	aat	act	1064
Lys	Ile	Leu	Lys	Leu	Pro	Leu	Leu	Val	Lys	Lys	Gln	Glu	Asn	Asn	Thr	
		325					330					335				
tat	atc	aac	gct	aat	ggc	gct	aag	ggt	aag	ata	gat	gaa	aaa	ggt	tat	1112
Tyr	Ile	Asn	Ala	Asn	Gly	Ala	Lys	Gly	Lys	Ile	Asp	Glu	Lys	Gly	Tyr	
	340					345					350					
ttg	gcc	aac	gct	ctc	aaa	aac	tat	gat	gag	act	ctt	gtg	gaa	gct	ttt	1160
Leu	Ala	Asn	Ala	Leu	Lys	Asn	Tyr	Asp	Glu	Thr	Leu	Val	Glu	Ala	Phe	
355					360					365					370	
atg	aga	gat	ttc	aag	gaa	cgc	tat	aag	ata	gaa	aaa	cta	tat	tat	tta	1208
Met	Arg	Asp	Phe	Lys	Glu	Arg	Tyr	Lys	Ile	Glu	Lys	Leu	Tyr	Tyr	Leu	
				375					380					385		
tta	gat	gat	aat	att	aaa	aat	ttt	gaa	ttt	gct	aag	atc	aag	cat	aaa	1256
Leu	Asp	Asp	Asn	Ile	Lys	Asn	Phe	Glu	Phe	Ala	Lys	Ile	Lys	His	Lys	
			390					395					400			
ata	agc	ttg	tat	ttt	aaa	gac	gca	aaa	ttc	tat	cct	aaa	agc	gtt	gct	1304
Ile	Ser	Leu	Tyr	Phe	Lys	Asp	Ala	Lys	Phe	Tyr	Pro	Lys	Ser	Val	Ala	
		405					410					415				
tta	gga	ttt	agt	tct	ttg	ttt	gaa	aat	aaa	tta	aag	aaa	aat	gag	cgt	1352
Leu	Gly	Phe	Ser	Ser	Leu	Phe	Glu	Asn	Lys	Leu	Lys	Lys	Asn	Glu	Arg	
	420					425					430					
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Leu	Arg	Tyr	Asn	Ser	Val	Asp	Leu	Val	Val	Lys	Glu	Asn	His	Lys	Ser	
	435				440				445					450		
aag	acc	ttt	aat	gat	tgt	ggc	ttg	gtt	ttg	gag	agg	caa	aaa	agc	gat	1448
Lys	Thr	Phe	Asn	Asp	Cys	Gly	Leu	Val	Leu	Glu	Arg	Gln	Lys	Ser	Asp	
				455				460						465		
gat	tca	aaa	gag	ttc	ctt	att	cta	caa	gat	tct	ttt	atc	aaa	aaa	gct	1496
Asp	Ser	Lys	Glu	Phe	Leu	Ile	Leu	Gln	Asp	Ser	Phe	Ile	Lys	Lys	Ala	
			470					475					480			
tta	aaa	aat	ttt	aaa	aga	gcc	tta	gga	tta	gaa	aaa	gaa	ggc	ttt	att	1544
Leu	Lys	Asn	Phe	Lys	Arg	Ala	Leu	Gly	Leu	Glu	Lys	Glu	Gly	Phe	Ile	
		485					490					495				
ctg	tat	aaa	gaa	tgc	ttg	cct	aag	ctc	tct	atg	gaa	gtg	gtt	aaa	gac	1592
Leu	Tyr	Lys	Glu	Cys	Leu	Pro	Lys	Leu	Ser	Met	Glu	Val	Val	Lys	Asp	
	500					505					510					

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cga Arg	gaa Glu	agt Ser	ttt Phe 550	gct Ala	ttg Leu	ccc Pro	ttg Leu	atc Ile 555	cta Leu	aat Asn	gaa Glu	gaa Glu	aaa Lys 560	atc Ile	gcc Ala	1736
tat Tyr	caa Gln	ggg Gly 565	aaa Lys	atc Ile	acc Thr	tct Ser	aaa Lys 570	gat Asp	ttt Phe	ccc Pro	cta Leu	gaa Glu 575	aat Asn	gac Asp	gaa Glu	1784
gaa Glu	tac Tyr 580	aaa Lys	ctc Leu	acg Thr	ctc Leu	act Thr 585	tat Tyr	gac Asp	att Ile	ggc Gly 590	acc Thr	gag Glu	ttt Phe	aac Asn	tat Tyr	1832
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gaa Glu	tgg Trp	cag Gln	cgt Arg	att Ile 615	gat Asp	agg Arg	gtt Val	gaa Glu	ctc Leu 620	cct Pro	acg Thr	ccc Pro	gat Asp	tcc Ser 625	atc Ile	1928
aaa Lys	aaa Lys	cca Pro	agt Ser 630	att Ile	gat Asp	gaa Glu	cta Leu	aaa Lys 635	aat Asn	gac Asp	ttt Phe	aat Asn	cct Pro 640	aaa Lys	agg Arg	1976
ggc Gly	aaa Lys 645	agt Ser	tct Ser	gat Asp	ttg Leu	ttt Phe	gag Glu 650	tgg Trp	gcg Ala	cta Leu	gag Glu	caa Gln 655	tta Leu	gag Glu	aca Thr	2024
ttg Leu 660	aaa Lys	gat Asp	tta Leu	aat Asn	agt Ser	cca Pro 665	ccc Pro	aga Arg	ttt Phe	gtt Val 670	tta Leu	gag Glu	aaa Lys	aaa Lys	cta Leu	2072
gaa Glu 675	tgc Cys	ggg Gly	gga Gly	atc Ile	tca Ser 680	ata Ile	ata Ile	ggg Gly	gaa Glu	gat Asp 685	aga Arg	aac Asn	aat Asn	gaa Glu	ctt Leu 690	2120
ttt Phe	tac Tyr	ata Ile	atg Met	gaa Glu 695	aca Thr	aat Asn	ggg Gly	aaa Lys	aaa Lys 700	gtt Val	ttt Phe	tgt Cys	cat His	agc Ser 705	cgt Arg	2168
caa Gln	tgc Cys	aaa Lys 710	ggg Gly	agc Ser	gtg Val	aac Asn	aaa Lys	gat Asp 715	gag Glu	ctt Leu	tca Ser	tta Leu	ggc Gly 720	gcg Ala	cga Arg	2216
gtg Val	tgt Cys	ttg Leu 725	gaa Glu	gtg Val	ggg Gly	cca Pro	gat Asp 730	aag Lys	aac Asn	gac Asp	cat His	ggg Gly 735	aaa Lys	tat Tyr	cga Arg	2264
ggg Gly	aaa Lys 740	att Ile	tat Tyr	ggg Gly	ttg Leu	gaa Glu 745	aaa Lys	aat Asn	aga Arg	gaa Glu	att Ile 750	gtt Val	tta Leu	tta Leu	aat Asn	2312



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755 760 765 770	
cac aga ata gaa gcg ctc aaa aga atc aag tat cct tgt tta aaa att	2408
His Arg Ile Glu Ala Leu Lys Arg Ile Lys Tyr Pro Cys Leu Lys Ile	
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Phe Ser His Tyr Met Leu Glu Glu Leu Glu Thr Leu Asn Pro Glu Phe	
790 795 800	
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Ala Thr Pro Phe Lys Glu Tyr Leu Lys Arg Leu Glu Glu Tyr Tyr Phe	
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Asp Pro Gln Thr Asp Arg Asp Phe Lys Lys Gly Leu Leu Asp Phe Phe	
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Ser Arg Leu Asn Asp Ser Ile Pro Ala Lys Leu Gln Gln Glu Phe Ile	
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Asn Leu Pro Ser Thr Asp Phe Leu Ser Arg Cys Leu Gly Ser Leu Glu	
855 860 865	
aaa gac ttt caa aaa acg att ttt aag aag ctt aaa gtt act aac cta	2696
Lys Asp Phe Gln Lys Thr Ile Phe Lys Lys Leu Lys Val Thr Asn Leu	
870 875 880	
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Lys Thr Leu Ser Ile Val Ala Arg Ala Ser Trp Asn Asn Glu Lys Phe	
885 890 895	
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Leu Glu Asn Leu Met Ala Gln Thr Ser Leu Glu Gln Lys Asp Phe	
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Ser Ser Ala Cys Glu Leu Leu Leu Ala Phe Leu Ser Tyr Arg Asn Ala	
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965 970 975	
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Phe Val Lys Leu Glu Leu Lys Asn Gln Ser Phe Asn Asn Ile Pro Pro	

980

985

990

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gga att gaa att aat ggg aca gaa gag gat gaa taaatcaaac aaattagtc 3133  
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 Ser Phe Glu Tyr Arg Asp Leu Phe Ser Val Leu Glu Asn Ile Val Gln  
 35 40 45  
 Phe Asp Tyr Glu Lys Lys Pro Tyr Lys Asp Asp Leu Tyr Phe Leu Cys  
 50 55 60  
 Lys Phe Val Glu Pro Ala Leu Lys Ala Ile Phe Ser Asn Leu Asn Thr  
 65 70 75 80  
 Asn Ile Tyr Arg Lys His Leu Lys Met Pro Leu Glu Lys Ala Arg Glu  
 85 90 95  
 Phe Asp Ala Lys Cys Ala Leu Asp Leu Ala Lys Arg Pro Gly Arg Ser  
 100 105 110  
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 115 120 125  
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 Phe Glu Glu Leu Ile Phe Ser Ile Thr Ser Phe Leu Lys Asn Gly Val  
 165 170 175  
 Ala Gln Gln Ile Asp Glu Lys Gln Ala Ile Ile Pro Asn Asn Leu Leu  
 180 185 190  
 His Phe Asp Lys His Tyr Lys Arg Ile Phe Lys Ala His Asp Trp Leu  
 195 200 205  
 Tyr Asp Gly Val Gly Ser Leu Met Asn Leu Asp Gln Ile Phe Tyr Leu  
 210 215 220  
 Glu Cys Leu Tyr Gln Ala Gln Phe Tyr Thr Ser Lys Asn Ile Glu Pro  
 225 230 235 240  
 Thr Leu Ile Arg Asn Glu Gln Asp Leu Tyr Ala Leu Ile Lys Asn Ser  
 245 250 255  
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 260 265 270  
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 275 280 285  
 Ile Pro Gln Leu Glu Leu Cys Lys Gly Val Tyr Lys Glu Met Tyr Ile  
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00695913-062901

106290.2165860

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Ala	Phe	Met	Arg	Asp	Phe	Lys	Glu	Arg	Tyr	Lys	Ile	Glu	Lys	Leu	Tyr			
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Tyr	Leu	Leu	Asp	Asp	Asn	Ile	Lys	Asn	Phe	Glu	Phe	Ala	Lys	Ile	Lys			
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His	Lys	Ile	Ser	Leu	Tyr	Phe	Lys	Asp	Ala	Lys	Phe	Tyr	Pro	Lys	Ser			
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Glu	Arg	Leu	Arg	Tyr	Asn	Ser	Val	Asp	Leu	Val	Val	Lys	Glu	Asn	His			
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Lys	Ser	Lys	Thr	Phe	Asn	Asp	Cys	Gly	Leu	Val	Leu	Glu	Arg	Gln	Lys			
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Val	Met	Glu	Trp	Gln	Arg	Ile	Asp	Arg	Val	Glu	Leu	Pro	Thr	Pro	Asp			
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Glu	Thr	Leu	Lys	Asp	Leu	Asn	Ser	Pro	Pro	Arg	Phe	Val	Leu	Glu	Lys			
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Ala	Arg	Val	Cys	Leu	Glu	Val	Gly	Pro	Asp	Lys	Asn	Asp	His	Gly	Lys			
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Leu	Asn	Thr	Ala	Lys	Asn	Ser	Tyr	Gln	Arg	Lys	Pro	Leu	Asp	Glu	Lys			
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Ile	Lys	His	Arg	Ile	Glu	Ala	Leu	Lys	Arg	Ile	Lys	Tyr	Pro	Cys	Leu			
	770					775					780							
Lys	Ile	Phe	Ser	His	Tyr	Met	Leu	Glu	Glu	Leu	Glu	Thr	Leu	Asn	Pro			
785					790					795					800			

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Glu Phe Ala Thr Pro Phe Lys Glu Tyr Leu Lys Arg Leu Glu Glu Tyr  
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Tyr Phe Asp Pro Gln Thr Asp Arg Asp Phe Lys Lys Gly Leu Leu Asp  
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Phe Phe Ser Arg Leu Asn Asp Ser Ile Pro Ala Lys Leu Gln Gln Glu  
835 840 845  
Phe Ile Asn Leu Pro Ser Thr Asp Phe Leu Ser Arg Cys Leu Gly Ser  
850 855 860  
Leu Glu Lys Asp Phe Gln Lys Thr Ile Phe Lys Lys Leu Lys Val Thr  
865 870 875 880  
Asn Leu Lys Thr Leu Ser Ile Val Ala Arg Ala Ser Trp Asn Asn Glu  
885 890 895  
Lys Phe Leu Glu Asn Leu Met Ala Gln Thr Ser Leu Glu Gln Gln Lys  
900 905 910  
Asp Phe Leu Lys Arg Ile Glu Glu Cys Leu Lys Asn Pro Glu Ser Phe  
915 920 925  
Tyr Phe Ser Ser Ala Cys Glu Leu Leu Leu Ala Phe Leu Ser Tyr Arg  
930 935 940  
Asn Ala Lys Arg Glu Leu Glu Leu Ile Pro Glu Ser Glu Lys Thr Met  
945 950 955 960  
Arg Leu Leu Asp Ser Ile Asp Lys Ala Ile Glu Lys Glu Thr Glu Ile  
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Lys Ser Phe Val Lys Leu Glu Leu Lys Asn Gln Ser Phe Asn Asn Ile  
980 985 990  
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agt ttt gtc atc aaa atg aag ttt ttt aaa gaa aaa gaa aaa gaa gtt 96  
Ser Phe Val Ile Lys Met Lys Phe Phe Lys Glu Lys Glu Lys Glu Val  
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tca aaa att aaa agt ttg aga aag ttt gag tca aat ccg cta gta aga 144  
Ser Lys Ile Lys Ser Leu Arg Lys Phe Glu Ser Asn Pro Leu Val Arg  
35 40 45  
  
ttt gac cct agc gct ctt gcg cta gag cca aaa ttt tagtataatg 190  
Phe Asp Pro Ser Ala Leu Ala Leu Glu Pro Lys Phe  
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<210> 342

[illegible]

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Ser	Lys	Ile 35	Lys	Ser	Leu	Arg	Lys 40	Phe	Glu	Ser	Asn 45	Pro	Leu	Val	Arg
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-401-

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gac aac aaa tca aaa tca tta att tta aaa aaa gcc gct aag acc gtt Asp Asn Lys Ser Lys Ser Leu Ile Leu Lys Lys Ala Ala Lys Thr Val 195 200 205 210	680
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Pro Phe Phe Pro Gly Asn Asn Lys Arg Thr Lys Ile Ile Pro Ala Glu 50 55 60	
Ile Lys Val Leu Arg Met Ser Lys Leu Thr Leu Glu Ser Leu Leu Pro 65 70 75 80	
Arg Ile Val Arg Ile Lys Ser Met Gly Met Ala Ala Ile Ser Trp Lys 85 90 95	
Ile Lys Ile Pro Thr Ala Leu Phe Pro Met Gly Val Leu Ser Cys Leu 100 105 110	
Glu Ser Ser Lys Asn Phe Ser Thr Ile Ala Val Glu Glu Ser Glu Ser 115 120 125	
Pro Met Pro Lys Thr Arg Glu Lys Met Gly Glu Arg Pro Lys Thr Lys 130 135 140	
Tyr Pro Asn Lys Lys Ala Ile Lys Ala His Lys Thr Thr Cys Lys Ser 145 150 155 160	
Pro Lys Thr Ser Thr Ser Cys Leu Met Asp Leu Ser Leu Ser Lys Leu 165 170 175	
Asn Ser Met Pro Ile Ile Asn Ile Lys Lys Thr Ile Pro Asn Ser Pro 180 185 190	
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Thr Val Pro Val Gln Met  
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Leu Glu Asn Leu Ser Gln Gln Lys Ile Leu Gln Leu Ser Gly Gly Gln  
5 10 15  
  
gcc caa cga gtc gct tta gca aga gct tta atc gca gcc aag aat cta 152  
Ala Gln Arg Val Ala Leu Ala Arg Ala Leu Ile Ala Ala Lys Asn Leu  
20 25 30  
  
ttg ctt tta gat gag cct tta aac gcc tta gat aac gcc tta aaa aac 200  
Leu Leu Leu Asp Glu Pro Leu Asn Ala Leu Asp Asn Ala Leu Lys Asn  
35 40 45 50  
  
gaa gtg caa caa ggt ttg ctt gat ttt atc aag cgt gaa aat tta agc 248  
Glu Val Gln Gln Gly Leu Leu Asp Phe Ile Lys Arg Glu Asn Leu Ser  
55 60 65  
  
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Val Leu Leu Val Ser His Asn Pro Asn Glu Ile Thr Lys Leu Ala Gln  
70 75 80  
  
act ttc ctc ttt tta aac aat ggc gtt att gat cct aat caa gaa aat 344  
Thr Phe Leu Phe Leu Asn Asn Gly Val Ile Asp Pro Asn Gln Glu Asn  
85 90 95  
  
cgg ctt ttt tca aac cgc tta tta ata aaa cct ctc ttt gaa gat gaa 392  
Arg Leu Phe Ser Asn Arg Leu Leu Ile Lys Pro Leu Phe Glu Asp Glu  
100 105 110  
  
aat tat tgc cat tat gag gtc att tct caa acg att agt ttg ccc aaa 440  
Asn Tyr Cys His Tyr Glu Val Ile Ser Gln Thr Ile Ser Leu Pro Lys  
115 120 125 130  
  
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Asp Cys Leu Asn Pro Thr Phe Lys Leu Asp Phe Asn Gln Asn Lys Lys  
135 140 145  
  
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**SECRET**

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Leu	Ile	Val	Thr	Arg	Phe	Ala	Pro	Ser	Pro	Thr	Gly	Tyr	Leu	His	Ile			
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Gly	Gly	Leu	Arg	Thr	Ala	Ile	Phe	Asn	Tyr	Leu	Phe	Ala	Arg	Ala	Asn			
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caa	gga	aaa	ttt	ttt	tta	cgc	att	gaa	gac	acg	gat	ttg	agc	cgt	aac			201
Gln	Gly	Lys	Phe	Phe	Leu	Arg	Ile	Glu	Asp	Thr	Asp	Leu	Ser	Arg	Asn			
	35				40					45					50			
tct	ata	gaa	gcg	gct	aac	gcc	att	ata	gaa	gct	ttc	aaa	tgg	gta	ggg			249
Ser	Ile	Glu	Ala	Ala	Asn	Ala	Ile	Ile	Glu	Ala	Phe	Lys	Trp	Val	Gly			
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cta	gaa	tac	gat	ggc	gaa	atc	ctc	tac	caa	tcc	aaa	cgc	ttt	gag	att			297
Leu	Glu	Tyr	Asp	Gly	Glu	Ile	Leu	Tyr	Gln	Ser	Lys	Arg	Phe	Glu	Ile			
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tat	aaa	gaa	tac	att	caa	aaa	ctc	tta	gat	gaa	gac	aaa	gcc	tat	tat			345



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Cys	Tyr	Met	Ser	Lys	Glu	Glu	Leu	Asp	Ala	Leu	Arg	Glu	Glu	Gln	Lys		
		100				105					110						
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Ala	Arg	Lys	Glu	Thr	Pro	Arg	Tyr	Asp	Asn	Arg	Tyr	Arg	Asp	Phe	Lys		
115					120					125					130		
ggc	acg	cct	cct	aaa	ggc	ata	gag	cct	gtg	gta	agg	att	aaa	gtc	ccc		489
Gly	Thr	Pro	Pro	Lys	Gly	Ile	Glu	Pro	Val	Val	Arg	Ile	Lys	Val	Pro		
				135					140					145			
caa	aat	gag	gtg	att	ggt	ttt	aat	gac	ggg	gtt	aaa	ggc	gaa	gtg	aaa		537
Gln	Asn	Glu	Val	Ile	Gly	Phe	Asn	Asp	Gly	Val	Lys	Gly	Glu	Val	Lys		
			150					155					160				
gtg	aat	act	aac	gaa	tta	gac	gat	ttt	att	atc	gcc	agg	agc	gat	ggg		585
Val	Asn	Thr	Asn	Glu	Leu	Asp	Asp	Phe	Ile	Ile	Ala	Arg	Ser	Asp	Gly		
		165					170					175					
aca	ccc	act	tat	aac	ttt	gtg	gtt	act	att	gat	gac	gct	tta	atg	ggg		633
Thr	Pro	Thr	Tyr	Asn	Phe	Val	Val	Thr	Ile	Asp	Asp	Ala	Leu	Met	Gly		
		180				185					190						
att	act	gat	gtg	att	aga	ggc	gat	gat	cac	ctt	tct	aac	acc	cct	aaa		681
Ile	Thr	Asp	Val	Ile	Arg	Gly	Asp	Asp	His	Leu	Ser	Asn	Thr	Pro	Lys		
195					200					205					210		
caa	atc	gtt	ctt	tat	aag	gct	ttg	aat	ttt	aaa	atc	cct	aat	ttt	ttc		729
Gln	Ile	Val	Leu	Tyr	Lys	Ala	Leu	Asn	Phe	Lys	Ile	Pro	Asn	Phe	Phe		
				215					220					225			
cat	gtg	ccg	atg	att	ttg	aat	gaa	gaa	ggg	caa	aaa	tta	agc	aaa	cgc		777
His	Val	Pro	Met	Ile	Leu	Asn	Glu	Glu	Gly	Gln	Lys	Leu	Ser	Lys	Arg		
			230				235						240				
cat	ggg	gcc	act	aat	gtg	atg	gac	tat	caa	gaa	atg	ggc	tat	ctt	aag		825
His	Gly	Ala	Thr	Asn	Val	Met	Asp	Tyr	Gln	Glu	Met	Gly	Tyr	Leu	Lys		
		245					250					255					
gaa	gct	tta	gtg	aat	ttt	tta	gcg	cgt	ttg	ggg	tgg	agc	tat	cag	gat		873
Glu	Ala	Leu	Val	Asn	Phe	Leu	Ala	Arg	Leu	Gly	Trp	Ser	Tyr	Gln	Asp		
		260				265					270						
aaa	gag	gtt	ttt	agc	atg	caa	gaa	ttg	cta	gaa	tta	ttt	gat	cct	aaa		921
Lys	Glu	Val	Phe	Ser	Met	Gln	Glu	Leu	Leu	Glu	Leu	Phe	Asp	Pro	Lys		
275					280					285					290		
gat	ttg	aat	tct	tcg	ccc	agt	tgc	ttc	agc	tgg	cac	aag	ctt	aat	tgg		969
Asp	Leu	Asn	Ser	Ser	Pro	Ser	Cys	Phe	Ser	Trp	His	Lys	Leu	Asn	Trp		
				295					300					305			
ctc	aac	gct	cat	tat	tta	aaa	aac	caa	agt	gtg	caa	gaa	ttg	tta	aaa		1017
Leu	Asn	Ala	His	Tyr	Leu	Lys	Asn	Gln	Ser	Val	Gln	Glu	Leu	Leu	Lys		
			310					315					320				

ctt tta aag cct ttt agt ttt agc gat ctc tcg cat tta aac ccc act 1065  
 Leu Leu Lys Pro Phe Ser Phe Ser Asp Leu Ser His Leu Asn Pro Thr  
 325 330 335

caa ttg gat cgc ttg tta gac gct ctc aaa gaa aga tct caa aca cta 1113  
 Gln Leu Asp Arg Leu Leu Asp Ala Leu Lys Glu Arg Ser Gln Thr Leu  
 340 345 350

aaa gaa tta gcc ctt aaa ata gat gag gtt tta atc gcc cct gtg gag 1161  
 Lys Glu Leu Ala Leu Lys Ile Asp Glu Val Leu Ile Ala Pro Val Glu  
 355 360 365 370

tat gaa gaa aag gtt ttt aaa aaa ctc aat caa gcg ctc gtt atg ccc 1209  
 Tyr Glu Glu Lys Val Phe Lys Lys Leu Asn Gln Ala Leu Val Met Pro  
 375 380 385

ttg tta gaa aag ttt aag cta gaa tta aac aaa gcc aat ttc aac gat 1257  
 Leu Leu Glu Lys Phe Lys Leu Glu Leu Asn Lys Ala Asn Phe Asn Asp  
 390 395 400

gaa agc gcg cta gaa aac gcc atg cgc caa atc att gaa gaa gaa aag 1305  
 Glu Ser Ala Leu Glu Asn Ala Met Arg Gln Ile Ile Glu Glu Glu Lys  
 405 410 415

att aaa gcg ggt agt ttt atg cag cct tta aga ttg gcc ctt ttg ggt 1353  
 Ile Lys Ala Gly Ser Phe Met Gln Pro Leu Arg Leu Ala Leu Leu Gly  
 420 425 430

aag gga ggc ggg ata ggc ctt aaa gaa gcg ctt ttt att tta ggc aaa 1401  
 Lys Gly Gly Gly Ile Gly Leu Lys Glu Ala Leu Phe Ile Leu Gly Lys  
 435 440 445 450

aca gag agc gtc aaa aga ata gag gat ttt ttg aaa aac taaaaaattg 1450  
 Thr Glu Ser Val Lys Arg Ile Glu Asp Phe Leu Lys Asn  
 455 460

gctctgtttt cattgggtat taaaataaaaa gagtttgatt ttagcggttg ttaagcaact 1510  
 ccttttgaaa aataagaggg 1530

<210> 348

<211> 463

<212> PRT

<213> Helicobacter pylori

<400> 348

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 His Ile Gly Gly Leu Arg Thr Ala Ile Phe Asn Tyr Leu Phe Ala Arg  
 20 25 30  
 Ala Asn Gln Gly Lys Phe Phe Leu Arg Ile Glu Asp Thr Asp Leu Ser  
 35 40 45  
 Arg Asn Ser Ile Glu Ala Ala Asn Ala Ile Ile Glu Ala Phe Lys Trp  
 50 55 60  
 Val Gly Leu Glu Tyr Asp Gly Glu Ile Leu Tyr Gln Ser Lys Arg Phe  
 65 70 75 80  
 Glu Ile Tyr Lys Glu Tyr Ile Gln Lys Leu Leu Asp Glu Asp Lys Ala  
 85 90 95  
 Tyr Tyr Cys Tyr Met Ser Lys Glu Glu Leu Asp Ala Leu Arg Glu Glu  
 100 105 110

Gln	Lys	Ala	Arg	Lys	Glu	Thr	Pro	Arg	Tyr	Asp	Asn	Arg	Tyr	Arg	Asp
		115					120					125			
Phe	Lys	Gly	Thr	Pro	Pro	Lys	Gly	Ile	Glu	Pro	Val	Val	Arg	Ile	Lys
		130				135					140				
Val	Pro	Gln	Asn	Glu	Val	Ile	Gly	Phe	Asn	Asp	Gly	Val	Lys	Gly	Glu
145				150					155						160
Val	Lys	Val	Asn	Thr	Asn	Glu	Leu	Asp	Asp	Phe	Ile	Ile	Ala	Arg	Ser
				165				170						175	
Asp	Gly	Thr	Pro	Thr	Tyr	Asn	Phe	Val	Val	Thr	Ile	Asp	Asp	Ala	Leu
			180				185					190			
Met	Gly	Ile	Thr	Asp	Val	Ile	Arg	Gly	Asp	Asp	His	Leu	Ser	Asn	Thr
		195					200				205				
Pro	Lys	Gln	Ile	Val	Leu	Tyr	Lys	Ala	Leu	Asn	Phe	Lys	Ile	Pro	Asn
		210				215					220				
Phe	Phe	His	Val	Pro	Met	Ile	Leu	Asn	Glu	Glu	Gly	Gln	Lys	Leu	Ser
225					230				235						240
Lys	Arg	His	Gly	Ala	Thr	Asn	Val	Met	Asp	Tyr	Gln	Glu	Met	Gly	Tyr
				245				250						255	
Leu	Lys	Glu	Ala	Leu	Val	Asn	Phe	Leu	Ala	Arg	Leu	Gly	Trp	Ser	Tyr
			260				265						270		
Gln	Asp	Lys	Glu	Val	Phe	Ser	Met	Gln	Glu	Leu	Leu	Glu	Leu	Phe	Asp
		275					280					285			
Pro	Lys	Asp	Leu	Asn	Ser	Ser	Pro	Ser	Cys	Phe	Ser	Trp	His	Lys	Leu
		290				295					300				
Asn	Trp	Leu	Asn	Ala	His	Tyr	Leu	Lys	Asn	Gln	Ser	Val	Gln	Glu	Leu
305					310				315						320
Leu	Lys	Leu	Leu	Lys	Pro	Phe	Ser	Phe	Ser	Asp	Leu	Ser	His	Leu	Asn
				325					330					335	
Pro	Thr	Gln	Leu	Asp	Arg	Leu	Leu	Asp	Ala	Leu	Lys	Glu	Arg	Ser	Gln
			340					345					350		
Thr	Leu	Lys	Glu	Leu	Ala	Leu	Lys	Ile	Asp	Glu	Val	Leu	Ile	Ala	Pro
		355					360					365			
Val	Glu	Tyr	Glu	Glu	Lys	Val	Phe	Lys	Lys	Leu	Asn	Gln	Ala	Leu	Val
		370				375					380				
Met	Pro	Leu	Leu	Glu	Lys	Phe	Lys	Leu	Glu	Leu	Asn	Lys	Ala	Asn	Phe
385					390					395					400
Asn	Asp	Glu	Ser	Ala	Leu	Glu	Asn	Ala	Met	Arg	Gln	Ile	Ile	Glu	Glu
				405					410					415	
Glu	Lys	Ile	Lys	Ala	Gly	Ser	Phe	Met	Gln	Pro	Leu	Arg	Leu	Ala	Leu
			420				425						430		
Leu	Gly	Lys	Gly	Gly	Gly	Ile	Gly	Leu	Lys	Glu	Ala	Leu	Phe	Ile	Leu
		435					440					445			
Gly	Lys	Thr	Glu	Ser	Val	Lys	Arg	Ile	Glu	Asp	Phe	Leu	Lys	Asn	
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<210> 349
<211> 382
<212> DNA
<213> Helicobacter pylori
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<220>  
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cctaattgatt ttttctatct tgccccctt atgtgttaga aaattctaaa atg ttt  
Met Phe  
1

1

aag ggg att tat cct atg cgt aat ttt cct atc cac cat aat ggt ttt 104  
 Lys Gly Ile Tyr Pro Met Arg Asn Phe Pro Ile His His Asn Gly Phe  
           5                          10                          15

aaa cat gaa gtg tta gct cac atg cta aaa agg cat aaa gag cca ttt 152  
 Lys His Glu Val Leu Ala His Met Leu Lys Arg His Lys Glu Pro Phe  
           20                          25                          30

att tta agc tat aat gac tgc gaa ttt gta agg aat gct tat aaa gat 200  
 Ile Leu Ser Tyr Asn Asp Cys Glu Phe Val Arg Asn Ala Tyr Lys Asp  
           35                          40                          45                          50

ttt aaa att tta gaa cca tct tgg caa tac act atg gga caa ggc gag 248  
 Phe Lys Ile Leu Glu Pro Ser Trp Gln Tyr Thr Met Gly Gln Gly Glu  
                           55                          60                          65

atc aga atg ggt aaa aat cgc tta gaa aga ggc gat aat aac cat gtc 296  
 Ile Arg Met Gly Lys Asn Arg Leu Glu Arg Gly Asp Asn Asn His Val  
                           70                          75                          80

aaa caa tct cat gag tta ttg att atc aag gag taaaaatgca tattagcgaa 349  
 Lys Gln Ser His Glu Leu Leu Ile Ile Lys Glu  
                           85                          90

gtcaaaaactg ccttttaaaat cgctgatgta gaa 382

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 <212> PRT  
 <213> Helicobacter pylori

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 Met Phe Lys Gly Ile Tyr Pro Met Arg Asn Phe Pro Ile His His Asn  
   1                          5                          10                          15  
 Gly Phe Lys His Glu Val Leu Ala His Met Leu Lys Arg His Lys Glu  
                           20                          25                          30  
 Pro Phe Ile Leu Ser Tyr Asn Asp Cys Glu Phe Val Arg Asn Ala Tyr  
           35                          40                          45  
 Lys Asp Phe Lys Ile Leu Glu Pro Ser Trp Gln Tyr Thr Met Gly Gln  
           50                          55                          60  
 Gly Glu Ile Arg Met Gly Lys Asn Arg Leu Glu Arg Gly Asp Asn Asn  
   65                          70                          75                          80  
 His Val Lys Gln Ser His Glu Leu Leu Ile Ile Lys Glu  
                           85                          90

<210> 351  
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 <212> DNA  
 <213> Helicobacter pylori

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 ataggggtga ttatagcatt tatggggcaa aaaaagtaga atctgtatca agttttatta 180  
 ag atg cat gcg gta aaa tcc gct aaa tca agg agt gtt att atg gaa 227



aag act tta gag ggc gat ttg gcc acg cct att gga gtg tat cgt atc	344
Lys Thr Leu Glu Gly Asp Leu Ala Thr Pro Ile Gly Val Tyr Arg Ile	
85 90 95	
acg cag aaa tta gag cgc ttg gat caa tat tat ggc gtt ttg gct ttt	392
Thr Gln Lys Leu Glu Arg Leu Asp Gln Tyr Tyr Gly Val Leu Ala Phe	
100 105 110	
gta acg aat tac cct aat ttg tat gat acc ttg aaa aaa cgc acc ggg	440
Val Thr Asn Tyr Pro Asn Leu Tyr Asp Thr Leu Lys Lys Arg Thr Gly	
115 120 125 130	
cat ggc att tgg gtg cat gga atg cct tta aat ggc gat cgg aat gaa	488
His Gly Ile Trp Val His Gly Met Pro Leu Asn Gly Asp Arg Asn Glu	
135 140 145	
ttg aac acc aag ggc tgt att gcg att gaa aac ccg ctt tta agc tct	536
Leu Asn Thr Lys Gly Cys Ile Ala Ile Glu Asn Pro Leu Leu Ser Ser	
150 155 160	
tat gac aaa gtg tta aaa ggc gaa aaa gcg ttc ctc atc acc tat gaa	584
Tyr Asp Lys Val Leu Lys Gly Glu Lys Ala Phe Leu Ile Thr Tyr Glu	
165 170 175	
gac aag ttt ttc cca agc acc aaa gaa gaa ttg agc atg att tta agc	632
Asp Lys Phe Phe Pro Ser Thr Lys Glu Glu Leu Ser Met Ile Leu Ser	
180 185 190	
tcc ctt ttt caa tgg aaa gaa gcc tgg gct agg ggc gat ttt gaa cgc	680
Ser Leu Phe Gln Trp Lys Glu Ala Trp Ala Arg Gly Asp Phe Glu Arg	
195 200 205 210	
tac atg cgt ttt tat aac ccc aat ttc act cgc tat gac ggc atg aaa	728
Tyr Met Arg Phe Tyr Asn Pro Asn Phe Thr Arg Tyr Asp Gly Met Lys	
215 220 225	
ttt aac gct ttt aaa gag tat aaa aaa agg gtg ttt gca aaa aac gaa	776
Phe Asn Ala Phe Lys Glu Tyr Lys Lys Arg Val Phe Ala Lys Asn Glu	
230 235 240	
aaa aag aat atc gct ttt tcc tct atc aat gtg atc cct tac ccc aac	824
Lys Lys Asn Ile Ala Phe Ser Ser Ile Asn Val Ile Pro Tyr Pro Asn	
245 250 255	
tct cag aac aaa cgc ttg ttt tat gtg gtg ttt gac caa gat tat aaa	872
Ser Gln Asn Lys Arg Leu Phe Tyr Val Val Phe Asp Gln Asp Tyr Lys	
260 265 270	
gcc tac cag cat aac aag ctc tct tat agc tcc aat tct caa aaa gaa	920
Ala Tyr Gln His Asn Lys Leu Ser Tyr Ser Ser Asn Ser Gln Lys Glu	
275 280 285 290	
ctc tat ata gag att gaa aac aat caa gtg tct att ata atg gaa aaa	968
Leu Tyr Ile Glu Ile Glu Asn Asn Gln Val Ser Ile Ile Met Glu Lys	
295 300 305	
taagaaaaat agggcctttgt tttaattagg ataatctaag cggatttttc taa	1021

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<210> 355
<211> 990
<212> DNA
<213> Helicobacter pylori
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<400> 355

54

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5 10 15 20	
gtt tta tta ttg ccg ttt tca ctt tgt ata gct gat gaa tat att agc	150
Val Leu Leu Leu Pro Phe Ser Leu Cys Ile Ala Asp Glu Tyr Ile Ser	
25 30 35	
ata agt gat gat tgg gat gaa att gtg cga aat cat aag aca tat tat	198
Ile Ser Asp Asp Trp Asp Glu Ile Val Arg Asn His Lys Thr Tyr Tyr	
40 45 50	
ttt gaa aat ggt tta gac cat ttt aat caa ggc caa tac cag caa gcc	246
Phe Glu Asn Gly Leu Asp His Phe Asn Gln Gly Gln Tyr Gln Gln Ala	
55 60 65	
ttt aaa gat ttt aga ttg gcg caa gaa tac agc atc ggg ctt ggc agt	294
Phe Lys Asp Phe Arg Leu Ala Gln Glu Tyr Ser Ile Gly Leu Gly Ser	
70 75 80	
gtt tat tta gcc aaa atg tat ttg gag gga aag ggc gtg aaa gtg gat	342
Val Tyr Leu Ala Lys Met Tyr Leu Glu Gly Lys Gly Val Lys Val Asp	
85 90 95 100	
tac aaa aaa gca caa ttt tat gca gaa aac gct atc aaa ggg tat ggg	390
Tyr Lys Lys Ala Gln Phe Tyr Ala Glu Asn Ala Ile Lys Gly Tyr Gly	
105 110 115	
agc gga ttg tta ggg ggt gct ctt att tta gga cgc atg caa gca gaa	438
Ser Gly Leu Leu Gly Gly Ala Leu Ile Leu Gly Arg Met Gln Ala Glu	
120 125 130	
ggc tta ggg atg aaa aag gat ttg aaa caa gcg ctc aag act tat agg	486
Gly Leu Gly Met Lys Lys Asp Leu Lys Gln Ala Leu Lys Thr Tyr Arg	
135 140 145	
cat gtg gtt cgc atg ttt tct aat aaa agc aca aat ttt gct aac aat	534
His Val Val Arg Met Phe Ser Asn Lys Ser Thr Asn Phe Ala Asn Asn	
150 155 160	
ttt aga tta cca aac ctt gcg gaa ttt act agt atg ctt att gga tcg	582
Phe Arg Leu Pro Asn Leu Ala Glu Phe Thr Ser Met Leu Ile Gly Ser	
165 170 175 180	
cga ttc att gat ctt tca ggt ttg agc gcg aat cct ata aaa ttt gga	630
Arg Phe Ile Asp Leu Ser Gly Leu Ser Ala Asn Pro Ile Lys Phe Gly	
185 190 195	
aag aaa ttt gga ata ctt gtt aag aaa tcc act caa atc aaa gat aag	678
Lys Lys Phe Gly Ile Leu Val Lys Lys Ser Thr Gln Ile Lys Asp Lys	
200 205 210	
aca ctt ctt tgg gaa gat att gct gaa att tca agc aat att act tta	726
Thr Leu Leu Trp Glu Asp Ile Ala Glu Ile Ser Ser Asn Ile Thr Leu	
215 220 225	
ctc aaa caa caa atg ggg gag atc ctt tat agg att ggg atc gct tat	774

005591-062901



Leu Lys Gln Gln Met Gly Glu Ile Leu Tyr Arg Ile Gly Ile Ala Tyr  
 230 235 240

aaa gaa ggg ctt ggc act aga aag aaa aag gac agg gct aaa aaa ttc 822  
 Lys Glu Gly Leu Gly Thr Arg Lys Lys Lys Asp Arg Ala Lys Lys Phe  
 245 250 255 260

ctg caa aaa tcc gca gaa ttt ggc tat gaa aaa gcc atg gaa gct ctg 870  
 Leu Gln Lys Ser Ala Glu Phe Gly Tyr Glu Lys Ala Met Glu Ala Leu  
 265 270 275

tagtttttta atcaaacttg tatcaagctt gactgaatgg gttagaaaaa tccgcttaga 930  
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 <211> 276  
 <212> PRT  
 <213> Helicobacter pylori

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 20 25 30  
 Glu Tyr Ile Ser Ile Ser Asp Asp Trp Asp Glu Ile Val Arg Asn His  
 35 40 45  
 Lys Thr Tyr Tyr Phe Glu Asn Gly Leu Asp His Phe Asn Gln Gly Gln  
 50 55 60  
 Tyr Gln Gln Ala Phe Lys Asp Phe Arg Leu Ala Gln Glu Tyr Ser Ile  
 65 70 75 80  
 Gly Leu Gly Ser Val Tyr Leu Ala Lys Met Tyr Leu Glu Gly Lys Gly  
 85 90 95  
 Val Lys Val Asp Tyr Lys Lys Ala Gln Phe Tyr Ala Glu Asn Ala Ile  
 100 105 110  
 Lys Gly Tyr Gly Ser Gly Leu Leu Gly Gly Ala Leu Ile Leu Gly Arg  
 115 120 125  
 Met Gln Ala Glu Gly Leu Gly Met Lys Lys Asp Leu Lys Gln Ala Leu  
 130 135 140  
 Lys Thr Tyr Arg His Val Val Arg Met Phe Ser Asn Lys Ser Thr Asn  
 145 150 155 160  
 Phe Ala Asn Asn Phe Arg Leu Pro Asn Leu Ala Glu Phe Thr Ser Met  
 165 170 175  
 Leu Ile Gly Ser Arg Phe Ile Asp Leu Ser Gly Leu Ser Ala Asn Pro  
 180 185 190  
 Ile Lys Phe Gly Lys Lys Phe Gly Ile Leu Val Lys Lys Ser Thr Gln  
 195 200 205  
 Ile Lys Asp Lys Thr Leu Leu Trp Glu Asp Ile Ala Glu Ile Ser Ser  
 210 215 220  
 Asn Ile Thr Leu Leu Lys Gln Gln Met Gly Glu Ile Leu Tyr Arg Ile  
 225 230 235 240  
 Gly Ile Ala Tyr Lys Glu Gly Leu Gly Thr Arg Lys Lys Lys Asp Arg  
 245 250 255  
 Ala Lys Lys Phe Leu Gln Lys Ser Ala Glu Phe Gly Tyr Glu Lys Ala  
 260 265 270  
 Met Glu Ala Leu  
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<210> 357  
 <211> 2685

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<212> DNA  
<213> Helicobacter pylori

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1          5          10          15

gag aaa tta ctc acc cct gaa gcg aga aaa ctc tta gaa gaa gct aaa      96
Glu Lys Leu Leu Thr Pro Glu Ala Arg Lys Leu Leu Glu Glu Ala Lys
          20          25          30

gag agc gtt aaa gct tat aaa gac tgc gta tca aaa gct agg aat gaa      144
Glu Ser Val Lys Ala Tyr Lys Asp Cys Val Ser Lys Ala Arg Asn Glu
          35          40          45

aaa gag aaa aaa gaa tgc gag aaa tta ctc acg cct gaa gcg aaa aaa      192
Lys Glu Lys Lys Glu Cys Glu Lys Leu Leu Thr Pro Glu Ala Lys Lys
          50          55          60

ctt tta gag caa caa gtg cta gat tgt ttg aaa aac gct aaa acc gaa      240
Leu Leu Glu Gln Gln Val Leu Asp Cys Leu Lys Asn Ala Lys Thr Glu
          65          70          75          80

gct gat aaa aaa agg tgt gtc aaa gat ctc cct aaa gac ttg cag aaa      288
Ala Asp Lys Lys Arg Cys Val Lys Asp Leu Pro Lys Asp Leu Gln Lys
          85          90          95

aag gtt tta gct aaa gag agc gtt aag gct tat ttg gac tgc gta tca      336
Lys Val Leu Ala Lys Glu Ser Val Lys Ala Tyr Leu Asp Cys Val Ser
          100          105          110

aga gct agg aat gaa aaa gag aaa aaa gaa tgc gag aaa ttg ctc acc      384
Arg Ala Arg Asn Glu Lys Glu Lys Lys Glu Cys Glu Lys Leu Leu Thr
          115          120          125

cct gaa gcg aaa aaa ctt tta gaa gaa gcc aaa gag agt ctt aaa gct      432
Pro Glu Ala Lys Lys Leu Leu Glu Glu Ala Lys Glu Ser Leu Lys Ala
          130          135          140

tat aaa gac tgc ctc tct caa gct aga aat gaa gaa gaa agg aga gct      480
Tyr Lys Asp Cys Leu Ser Gln Ala Arg Asn Glu Glu Glu Arg Arg Ala
          145          150          155          160

tgc gag aaa cta ctc acg cct gaa gcg aga aaa ctc tta gag caa gaa      528
Cys Glu Lys Leu Leu Thr Pro Glu Ala Arg Lys Leu Leu Glu Gln Glu
          165          170          175

gtt aag aaa agc att aag gct tat ttg gac tgc gta tca aga gct agg      576
Val Lys Lys Ser Ile Lys Ala Tyr Leu Asp Cys Val Ser Arg Ala Arg
          180          185          190

aat gaa aaa gag aaa aaa gaa tgc gag aaa tta ctc acg cct gaa gcg      624
Asn Glu Lys Glu Lys Lys Glu Cys Glu Lys Leu Leu Thr Pro Glu Ala
          195          200          205

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09895913.062901

aga	aaa	ttt	tta	gcg	aag	caa	gtg	cta	aat	tgt	ttg	gaa	aaa	gct	gga	672
Arg	Lys	Phe	Leu	Ala	Lys	Gln	Val	Leu	Asn	Cys	Leu	Glu	Lys	Ala	Gly	
	210					215					220					
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Gln	Glu	Asn	Ile	Leu	Ala	Lys	Glu	Ser	Leu	Lys	Ala	Tyr	Lys	Asp	Cys	
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Leu	Ser	Gln	Ala	Arg	Asn	Glu	Glu	Glu	Arg	Arg	Ala	Cys	Glu	Lys	Leu	
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ctc	acg	cct	gaa	gcg	aga	aaa	ctc	tta	gag	caa	gaa	gtt	aag	aaa	agc	864
Leu	Thr	Pro	Glu	Ala	Arg	Lys	Leu	Leu	Glu	Gln	Glu	Val	Lys	Lys	Ser	
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Val	Lys	Ala	Tyr	Leu	Asp	Cys	Val	Ser	Arg	Ala	Arg	Asn	Glu	Lys	Glu	
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Lys	Lys	Glu	Cys	Glu	Lys	Leu	Leu	Thr	Pro	Glu	Ala	Arg	Lys	Phe	Leu	
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Ala	Lys	Glu	Leu	Gln	Gln	Lys	Asp	Lys	Ala	Ile	Lys	Asp	Cys	Leu	Lys	
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aac	gcc	gat	cct	aac	gac	aga	gcg	gct	atc	atg	aag	tgt	ttg	gat	ggt	1056
Asn	Ala	Asp	Pro	Asn	Asp	Arg	Ala	Ala	Ile	Met	Lys	Cys	Leu	Asp	Gly	
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Leu	Ser	Asp	Glu	Glu	Lys	Leu	Lys	Tyr	Leu	Gln	Glu	Ala	Arg	Glu	Lys	
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Ala	Val	Ala	Asp	Cys	Leu	Ala	Met	Ala	Lys	Thr	Asp	Glu	Glu	Lys	Arg	
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Lys	Cys	Gln	Asn	Leu	Tyr	Ser	Asp	Leu	Ile	Gln	Glu	Ile	Gln	Asn	Lys	
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Arg	Thr	Gln	Asn	Lys	Gln	Asn	Gln	Leu	Ser	Lys	Thr	Glu	Arg	Leu	His	

435	440	445	
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gat cta aga aac cgt aaa acc ttt gat aac atg gcg gct aaa ggt tat Asp Leu Arg Asn Arg Lys Thr Phe Asp Asn Met Ala Ala Lys Gly Tyr 465 470 475 480			1440
cca ttg tta cca atg gat ttc aaa aat ggc ggc gat att gcc act att Pro Leu Leu Pro Met Asp Phe Lys Asn Gly Gly Asp Ile Ala Thr Ile 485 490 495			1488
aac gcc act aat gtt gat gcg gac aaa ata gct agc gat aat cct att Asn Ala Thr Asn Val Asp Ala Asp Lys Ile Ala Ser Asp Asn Pro Ile 500 505 510			1536
tat gct tcc ata gag cct gat att gcc aag caa tac gaa aca gaa aaa Tyr Ala Ser Ile Glu Pro Asp Ile Ala Lys Gln Tyr Glu Thr Glu Lys 515 520 525			1584
acc att aag gat aag aat tta gaa gct aaa tta gct aag gct tta ggt Thr Ile Lys Asp Lys Asn Leu Glu Ala Lys Leu Ala Lys Ala Leu Gly 530 535 540			1632
ggc aat aaa aaa gat gac gat aaa gaa aaa agt aaa aaa tcc aca gca Gly Asn Lys Lys Asp Asp Asp Lys Glu Lys Ser Lys Lys Ser Thr Ala 545 550 555 560			1680
gaa gct aaa gca gaa aac aat aag ata gac aaa gat gtc gca gaa act Glu Ala Lys Ala Glu Asn Asn Lys Ile Asp Lys Asp Val Ala Glu Thr 565 570 575			1728
gcc aag aat atc agt gaa atc gct ctt aag aac aaa aaa gaa aag agt Ala Lys Asn Ile Ser Glu Ile Ala Leu Lys Asn Lys Lys Glu Lys Ser 580 585 590			1776
ggg gaa ttt gta gat gaa aat ggt aat ccc att gat gac aaa aag aaa Gly Glu Phe Val Asp Glu Asn Gly Asn Pro Ile Asp Asp Lys Lys Lys 595 600 605			1824
gca gaa aaa caa gat gaa aca agc cct gtc aaa cag gcc ttt ata ggc Ala Glu Lys Gln Asp Glu Thr Ser Pro Val Lys Gln Ala Phe Ile Gly 610 615 620			1872
aag agt gat ccc aca ttt gtt tta gcg caa tac acc ccc att gaa atc Lys Ser Asp Pro Thr Phe Val Leu Ala Gln Tyr Thr Pro Ile Glu Ile 625 630 635 640			1920
act ctg act tct aaa gta gat gcc act ctc aca ggt ata gtg agt ggg Thr Leu Thr Ser Lys Val Asp Ala Thr Leu Thr Gly Ile Val Ser Gly 645 650 655			1968
gtt gta gcc aaa gat gta tgg aac atg aac ggc act atg atc tta tta Val Val Ala Lys Asp Val Trp Asn Met Asn Gly Thr Met Ile Leu Leu 660 665 670			2016
gac aaa ggc act aag gtg tat ggg aat tat caa agc gtg aaa ggt ggc			2064

0055913-062901

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Thr	Pro	Ile	Met	Thr	Arg	Leu	Met	Ile	Val	Phe	Thr	Lys	Ala	Ile	Thr		
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cct	gat	ggg	gtg	ata	ata	cct	cta	gca	aac	gct	caa	gca	gca	ggc	atg	2160	
Pro	Asp	Gly	Val	Ile	Ile	Pro	Leu	Ala	Asn	Ala	Gln	Ala	Ala	Gly	Met		
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Thr	Ala	Pro	Ile	Ile	Ala	Leu	Asp	Lys	Leu	Ile	Gly	Leu	Gly	Lys	Gly		
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aga	agt	gaa	agg	aca	cct	gaa	ttt	aat	tac	gct	ttg	ggg	caa	gct	atc	2352	
Arg	Ser	Glu	Arg	Thr	Pro	Glu	Phe	Asn	Tyr	Ala	Leu	Gly	Gln	Ala	Ile		
		770				775					780						
aat	ggg	agc	atg	caa	agt	tca	gct	cag	atg	tct	aat	caa	att	cta	ggg	2400	
Asn	Gly	Ser	Met	Gln	Ser	Ser	Ala	Gln	Met	Ser	Asn	Gln	Ile	Leu	Gly		
		785			790					795					800		
caa	ctg	atg	aat	atc	ccc	cca	agt	ttt	tac	aaa	aac	gag	ggc	gat	agt	2448	
Gln	Leu	Met	Asn	Ile	Pro	Pro	Ser	Phe	Tyr	Lys	Asn	Glu	Gly	Asp	Ser		
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Ile	Lys	Ile	Leu	Thr	Met	Asp	Asp	Ile	Asp	Phe	Ser	Gly	Val	Tyr	Asp		
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gtt	aaa	att	act	aac	aaa	tct	gtg	gta	gat	gaa	att	atc	aaa	caa	agc	2544	
Val	Lys	Ile	Thr	Asn	Lys	Ser	Val	Val	Asp	Glu	Ile	Ile	Lys	Gln	Ser		
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acc	aaa	act	ttg	tct	aga	gaa	cat	gaa	gaa	atc	acc	aca	agc	ccc	aaa	2592	
Thr	Lys	Thr	Leu	Ser	Arg	Glu	His	Glu	Glu	Ile	Thr	Thr	Ser	Pro	Lys		
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Glu	Ser	Val	Lys	Ala	Tyr	Lys	Asp	Cys	Val	Ser	Lys	Ala	Arg	Asn	Glu
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Lys	Glu	Lys	Lys	Glu	Cys	Glu	Lys	Leu	Leu	Thr	Pro	Glu	Ala	Lys	Lys
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Leu	Leu	Glu	Gln	Gln	Val	Leu	Asp	Cys	Leu	Lys	Asn	Ala	Lys	Thr	Glu
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Ala	Asp	Lys	Lys	Arg	Cys	Val	Lys	Asp	Leu	Pro	Lys	Asp	Leu	Gln	Lys
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Lys	Val	Leu	Ala	Lys	Glu	Ser	Val	Lys	Ala	Tyr	Leu	Asp	Cys	Val	Ser
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Arg	Ala	Arg	Asn	Glu	Lys	Glu	Lys	Lys	Glu	Cys	Glu	Lys	Leu	Leu	Thr
		115					120					125			
Pro	Glu	Ala	Lys	Lys	Leu	Leu	Glu	Glu	Ala	Lys	Glu	Ser	Leu	Lys	Ala
	130					135					140				
Tyr	Lys	Asp	Cys	Leu	Ser	Gln	Ala	Arg	Asn	Glu	Glu	Glu	Arg	Arg	Ala
145				150					155					160	
Cys	Glu	Lys	Leu	Leu	Thr	Pro	Glu	Ala	Arg	Lys	Leu	Leu	Glu	Gln	Glu
			165						170					175	
Val	Lys	Lys	Ser	Ile	Lys	Ala	Tyr	Leu	Asp	Cys	Val	Ser	Arg	Ala	Arg
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Asn	Glu	Lys	Glu	Lys	Lys	Glu	Cys	Glu	Lys	Leu	Leu	Thr	Pro	Glu	Ala
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Arg	Lys	Phe	Leu	Ala	Lys	Gln	Val	Leu	Asn	Cys	Leu	Glu	Lys	Ala	Gly
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Asn	Glu	Glu	Glu	Arg	Lys	Ala	Cys	Leu	Lys	Asn	Leu	Pro	Lys	Asp	Leu
225					230					235				240	
Gln	Glu	Asn	Ile	Leu	Ala	Lys	Glu	Ser	Leu	Lys	Ala	Tyr	Lys	Asp	Cys
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Leu	Ser	Gln	Ala	Arg	Asn	Glu	Glu	Glu	Arg	Arg	Ala	Cys	Glu	Lys	Leu
			260					265					270		
Leu	Thr	Pro	Glu	Ala	Arg	Lys	Leu	Leu	Glu	Gln	Glu	Val	Lys	Lys	Ser
		275					280					285			
Val	Lys	Ala	Tyr	Leu	Asp	Cys	Val	Ser	Arg	Ala	Arg	Asn	Glu	Lys	Glu
	290					295					300				
Lys	Lys	Glu	Cys	Glu	Lys	Leu	Leu	Thr	Pro	Glu	Ala	Arg	Lys	Phe	Leu
305					310					315				320	
Ala	Lys	Glu	Leu	Gln	Lys	Asp	Lys	Ala	Ile	Lys	Asp	Cys	Leu	Lys	
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Asn	Ala	Asp	Pro	Asn	Asp	Arg	Ala	Ala	Ile	Met	Lys	Cys	Leu	Asp	Gly
			340					345					350		
Leu	Ser	Asp	Glu	Glu	Lys	Leu	Lys	Tyr	Leu	Gln	Glu	Ala	Arg		

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465		470		475		480									
Pro	Leu	Leu	Pro	Met	Asp	Phe	Lys	Asn	Gly	Gly	Asp	Ile	Ala	Thr	Ile
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Asn	Ala	Thr	Asn	Val	Asp	Ala	Asp	Lys	Ile	Ala	Ser	Asp	Asn	Pro	Ile
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Tyr	Ala	Ser	Ile	Glu	Pro	Asp	Ile	Ala	Lys	Gln	Tyr	Glu	Thr	Glu	Lys
		515					520					525			
Thr	Ile	Lys	Asp	Lys	Asn	Leu	Glu	Ala	Lys	Leu	Ala	Lys	Ala	Leu	Gly
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Gly	Asn	Lys	Lys	Asp	Asp	Asp	Lys	Glu	Lys	Ser	Lys	Lys	Ser	Thr	Ala
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Glu	Ala	Lys	Ala	Glu	Asn	Asn	Lys	Ile	Asp	Lys	Asp	Val	Ala	Glu	Thr
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Ala	Lys	Asn	Ile	Ser	Glu	Ile	Ala	Leu	Lys	Asn	Lys	Lys	Glu	Lys	Ser
		580						585					590		
Gly	Glu	Phe	Val	Asp	Glu	Asn	Gly	Asn	Pro	Ile	Asp	Asp	Lys	Lys	Lys
		595					600					605			
Ala	Glu	Lys	Gln	Asp	Glu	Thr	Ser	Pro	Val	Lys	Gln	Ala	Phe	Ile	Gly
	610					615					620				
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625					630					635					640
Thr	Leu	Thr	Ser	Lys	Val	Asp	Ala	Thr	Leu	Thr	Gly	Ile	Val	Ser	Gly
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Val	Val	Ala	Lys	Asp	Val	Trp	Asn	Met	Asn	Gly	Thr	Met	Ile	Leu	Leu
		660					665						670		
Asp	Lys	Gly	Thr	Lys	Val	Tyr	Gly	Asn	Tyr	Gln	Ser	Val	Lys	Gly	Gly
		675					680					685			
Thr	Pro	Ile	Met	Thr	Arg	Leu	Met	Ile	Val	Phe	Thr	Lys	Ala	Ile	Thr
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Pro	Asp	Gly	Val	Ile	Ile	Pro	Leu	Ala	Asn	Ala	Gln	Ala	Ala	Gly	Met
705					710					715					720
Leu	Gly	Glu	Ala	Gly	Val	Asp	Gly	Tyr	Val	Asn	Asn	His	Phe	Met	Lys
			725						730					735	
Arg	Ile	Gly	Phe	Ala	Val	Ile	Ala	Ser	Val	Val	Asn	Ser	Phe	Leu	Gln
		740					745					750			
Thr	Ala	Pro	Ile	Ile	Ala	Leu	Asp	Lys	Leu	Ile	Gly	Leu	Gly	Lys	Gly
		755				760					765				
Arg	Ser	Glu	Arg	Thr	Pro	Glu	Phe	Asn	Tyr	Ala	Leu	Gly	Gln	Ala	Ile
	770					775					780				
Asn	Gly	Ser	Met	Gln	Ser	Ser	Ala	Gln	Met	Ser	Asn	Gln	Ile	Leu	Gly
785					790					795					800
Gln	Leu	Met	Asn	Ile	Pro	Pro	Ser	Phe	Tyr	Lys	Asn	Glu	Gly	Asp	Ser
			805						810					815	
Ile	Lys	Ile	Leu	Thr	Met	Asp	Asp	Ile	Asp	Phe	Ser	Gly	Val	Tyr	Asp
		820						825					830		
Val	Lys	Ile	Thr	Asn	Lys	Ser	Val	Val	Asp	Glu	Ile	Ile	Lys	Gln	Ser
		835					840					845			
Thr	Lys	Thr	Leu	Ser	Arg	Glu	His	Glu	Glu	Ile	Thr	Thr	Ser	Pro	Lys
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Gly	Gly	Asn													
865															

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Met Ala Val Tyr Leu Asp Phe Glu Asn His Ile Lys Glu Ile Gln	
1 5 10 15	
aat gaa att gaa tta gcc ctt att aga ggc gat gag gac gct aaa gaa	157
Asn Glu Ile Glu Leu Ala Leu Ile Arg Gly Asp Glu Asp Ala Lys Glu	
20 25 30	
atc tta gaa aaa aga ttg gat aag gag gtt aaa agc att tat tcc aat	205
Ile Leu Glu Lys Arg Leu Asp Lys Glu Val Lys Ser Ile Tyr Ser Asn	
35 40 45	
ctc act gat ttt caa aaa ctc caa tta gca aga cac cct gac aga ccc	253
Leu Thr Asp Phe Gln Lys Leu Gln Leu Ala Arg His Pro Asp Arg Pro	
50 55 60	
tac gct atg gat tac att gat ctc atc tta aaa gat aaa tat gaa gtc	301
Tyr Ala Met Asp Tyr Ile Asp Leu Ile Leu Lys Asp Lys Tyr Glu Val	
65 70 75	
ttt ggg gat agg cat tat aac gat gat aaa gcg atc gtg tgc ttt gta	349
Phe Gly Asp Arg His Tyr Asn Asp Asp Lys Ala Ile Val Cys Phe Val	
80 85 90 95	
ggg aaa att gat aat gtc cca gtt gtg gtg atc gga gaa gaa aag ggc	397
Gly Lys Ile Asp Asn Val Pro Val Val Val Ile Gly Glu Glu Lys Gly	
100 105 110	
aga ggg act aaa aac aaa ctc tta aga aat ttt ggc atg cct aac cct	445
Arg Gly Thr Lys Asn Lys Leu Leu Arg Asn Phe Gly Met Pro Asn Pro	
115 120 125	
tgt ggc tat cgt aag gct ttg aaa atg gca aag ttt gct gaa aag ttt	493
Cys Gly Tyr Arg Lys Ala Leu Lys Met Ala Lys Phe Ala Glu Lys Phe	
130 135 140	
aat ttg cct att tta atg ctt gtg gat aca gcc ggg gcg tat ccg ggg	541
Asn Leu Pro Ile Leu Met Leu Val Asp Thr Ala Gly Ala Tyr Pro Gly	
145 150 155	
att ggt gca gaa gaa agg ggg caa agt gaa gcg atc gct aaa aat ctc	589
Ile Gly Ala Glu Glu Arg Gly Gln Ser Glu Ala Ile Ala Lys Asn Leu	
160 165 170 175	
caa gag ttc gcc tct tta aaa gtc cct act att tct gta att atc ggt	637
Gln Glu Phe Ala Ser Leu Lys Val Pro Thr Ile Ser Val Ile Ile Gly	
180 185 190	
gag ggg ggc agt ggt ggt gcg cta cga ttg cag tgg ctg aca aat tgg	685
Glu Gly Gly Ser Gly Gly Ala Leu Arg Leu Gln Trp Leu Thr Asn Trp	
195 200 205	
cta tgatggaata ttccattttt agcgttatat ccccagaagg ttgtgcggcg	738
attctttggg atgaccctag caagactgaa gtggctatta aagcgatgaa aatcacgcct	798
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Leu	Glu	Lys 35	Arg	Leu	Asp	Lys	Glu 40	Val	Lys	Ser	Ile	Tyr 45	Ser	Asn	Leu
Thr	Asp 50	Phe	Gln	Lys	Leu 55	Gln	Leu	Ala	Arg	His 60	Pro	Asp	Arg	Pro	Tyr
Ala 65	Met	Asp	Tyr	Ile 70	Asp	Leu	Ile	Leu	Lys	Asp 75	Lys	Tyr	Glu	Val	Phe 80
Gly	Asp	Arg	His 85	Tyr	Asn	Asp	Asp	Lys	Ala 90	Ile	Val	Cys	Phe 95	Val	Gly
Lys	Ile	Asp	Asn 100	Val	Pro	Val	Val	Val 105	Ile	Gly	Glu	Glu	Lys 110	Gly	Arg
Gly	Thr	Lys 115	Asn	Lys	Leu	Leu	Arg	Asn 120	Phe	Gly	Met	Pro	Asn 125	Pro	Cys
Gly	Tyr 130	Arg	Lys	Ala	Leu	Lys 135	Met	Ala	Lys	Phe 140	Ala	Glu	Lys	Phe	Asn
Leu 145	Pro	Ile	Leu	Met 150	Leu	Val	Asp	Thr	Ala	Gly 155	Ala	Tyr	Pro	Gly	Ile 160
Gly	Ala	Glu	Glu	Arg 165	Gly	Gln	Ser	Glu	Ala 170	Ile	Ala	Lys	Asn 175	Leu	Gln
Glu	Phe	Ala	Ser 180	Leu	Lys	Val	Pro	Thr 185	Ile	Ser	Val	Ile	Ile 190	Gly	Glu
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      Met Gln Phe Thr Gly Lys Asn Val Leu Ile Thr Gly Ala Ser
            1             5             10

aaa ggc att ggg gct gaa atc gcc aaa act ctc gct tct atg ggg ctg      156
Lys Gly Ile Gly Ala Glu Ile Ala Lys Thr Leu Ala Ser Met Gly Leu
      15             20             25             30

aaa gtt tgg atc aat tac cgc agt aat gct gaa gtg gct gac gct ttg      204
Lys Val Trp Ile Asn Tyr Arg Ser Asn Ala Glu Val Ala Asp Ala Leu
            35             40             45

aaa aat gag ctt gaa gaa aaa ggc tat aag gca gct gtc att aaa ttt      252

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Asp	Ala	Ala	Ser	Glu	Ser	Asp	Phe	Ile	Glu	Ala	Ile	Gln	Thr	Ile	Val	
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Ile	Asp	Asn	Asn	Leu	Thr	Ser	Ala	Phe	Ile	Gly	Cys	Arg	Glu	Ala	Leu	
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Lys	Val	Met	Ser	Lys	Ser	Arg	Phe	Gly	Ser	Val	Val	Asn	Val	Ala	Ser	
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Asn	Ile	Pro	Leu	Asn	Arg	Leu	Gly	Ser	Ala	Lys	Glu	Val	Ala	Glu	Ala	
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